

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using SW model.

Run on: August 10, 2004, 15:55:40 ; Search time 80.4324; Seconds

Title: US-10-072-602B-352  
Perfect score: 331  
Sequence: 1 MRCLFVFLVILLTASGPSV.....LQRHQDKSVCCGTYKLCFCPCG 62

Scoring table: BL0SUM62  
Gapext 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues  
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 20000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:  
1: GeneseqD1900s: \*  
2: GeneseqD2900s: \*  
3: GeneseqD2001s: \*  
4: GeneseqD2002s: \*  
5: GeneseqD2003s: \*  
6: GeneseqD2003bs: \*  
7: GeneseqD2003bs: \*  
8: GeneseqD2004s: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	331	100.0	62	5 ABG99600	Abg99600 Conus sp
2	298	90.0	62	5 ABG99591	Abg99591 Conus sp
3	286	86.4	62	5 ABG99589	Abg99589 Conus sp
4	281	84.9	62	5 ABG99517	Abg99517 Conus sp
5	281	84.9	62	5 ABG99614	Abg99614 Conus sp
6	272	82.2	64	5 ABG99593	Abg99593 Conus sp
7	266	80.4	62	5 ABG99606	Abg99606 Conus sp
8	264	79.8	64	5 ABG99470	Abg99470 Conus sp
9	264	79.8	64	5 ABG99587	Abg99587 Conus sp
10	264	79.8	64	5 ABG99608	Abg99608 Conus sp
11	254.5	76.9	61	5 ABG99561	Abg99561 Conus sp
12	253.5	76.6	61	5 ABG99612	Abg99612 Conus sp
13	220	65.5	60	5 ABG99569	Abg99569 Conus sp
14	216	65.3	61	5 ABG99400	Abg99400 Conus sp
15	216	65.3	61	5 ABG99598	Abg99598 Conus sp
16	211.5	63.9	61	5 ABG99551	Abg99551 Conus sp
17	208	62.8	61	5 ABG99571	Abg99571 Conus sp
18	206	62.2	59	3 AY97123	Aay97123 Tau conot
19	201.5	60.9	62	5 ABG99557	Abg99557 Conus sp
20	200	60.4	58	5 ABG99559	Abg99559 Conus sp
21	199	60.1	60	3 AY97124	Aay97124 Tau conot
22	199	60.1	70	3 AY97122	Aay97122 Tau conot
23	192	58.0	61	5 ABG99595	Abg99595 Conus sp
24	191	57.7	61	3 AAB08016	Aab08016 Amino aci
25	191	57.7	61	5 ABG99595	Abg99595 Conus sp

PS Claim 1, Page 239; 305pp; English.  
XX PT New cone snail conotoxin peptides, useful as a pain reliever for  
CC CC This invention describes novel conotoxin peptides from the cone snail,  
CC CC genus Conus which have analgesic activity and can act as a voltage-gated  
CC CC ion channel modulator or a ligand-gated ion channel modulator. The  
CC CC conotoxin peptide is useful as a pain-relieving agent for alleviating  
CC CC pain in an individual who is either exhibiting pain or is about to be  
CC CC subjected to a pain-causing event. The conotoxin peptide is also useful  
CC CC for treating or preventing disorders associated with voltage-gated ion  
CC CC channel disorders, ligand-gated ion channel disorders or receptor  
CC CC disorders. The radiolabeled conotoxin peptide is also useful for

26	189	57.1	61	3 AAY92231	Aay92231 Chi-conot
27	188	56.8	63	5 ABG90555	Abg90555 Conus sp
28	180.5	54.5	62	3 AAY97129	Aay97129 Tau conot
29	180	54.4	59	5 ABG99563	Abg99563 Conus sp
30	179	54.1	63	3 AAY97126	Aay97126 Tau conot
31	176	53.2	60	5 ABG99567	Abg99567 Conus sp
32	175	52.9	59	5 ABG99565	Abg99565 Conus sp
33	169.5	51.2	62	3 AAY97115	Aay97115 Tau conot
34	169	51.1	62	3 AAY97117	Aay97117 Tau conot
35	167.5	50.6	64	3 AAY97125	Aay97125 Tau conot
36	167	50.5	67	3 AAY97120	Aay97120 Tau conot
37	166	50.2	67	3 AAY97121	Aay97121 Tau conot
38	164	49.5	62	3 AAY97127	Aay97127 Tau conot
39	163.5	49.4	64	5 ABG99549	Abg99549 Conus sp
40	151.5	45.8	61	3 AAY97116	Aay97116 Tau conot
41	151.5	45.8	61	3 AAY97119	Aay97119 Tau conot
42	148	44.7	63	3 AAY97128	Aay97128 Tau conot
43	130	39.3	61	5 ABG99553	Abg99553 Conus sp
44	129.5	39.1	62	3 AAY97118	Aay97118 Tau conot
45	79	23.9	12	5 ABG99749	Abg99749 Conus sp

#### ALIGNMENTS

RESULT 1  
ID ABG99600 standard; protein; 62 AA.  
XX AC ABG99600;  
XX DT 17-JAN-2003 (first entry)  
XX DE DE  
XX KW Conotoxin; Cone snail; analgesic; voltage-gated ion channel modulator;  
KW ligand-gated ion channel modulator; pain-relief.  
XX OS Conus aulicus.  
XX PN WO200264740-A2.  
XX PD 22-AUG-2002.  
XX PP 11-FEB-2002; 2002WO-US003887.  
XX PR 09-FEB-2001; 2001US-0267408P.  
XX PA (COGNEX INC.  
PA (UTAH ) UNIV UTAH RES FOUND.  
XX PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz Lj,  
PI Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;  
XX DR WPI; 2002-706931/76.  
DR N-PSB; ABX04337.



Query Match	86.4%;	Score 286;	DB 5;	Length 62;	Qy	1 MRCLPVFVILLLTASGPSPYDARLTKTDDVPLSSFRDNASTLQRHQDKSVCVCGYKLCFP 60
Best Local Similarity	88.5%;	Pred. No. 3.2e-29;			Db	1 MHCLPPIFVILLLTASGPSPYDARLTKTDDVPLSSFRDNASTLQRHQDKSVCVCGYKLCFP 60
Matches 54; Conservative 3; Mismatches 4; Indels 0; Gaps 0;					Qy	61 CG 62
Qy	1 MRCLPVFVILLLTASGPSPYDARLTKTDDVPLSSFRDNASTLQRHQDKSVCVCGYKLCFP 60				Db	61 CG 62
Db	1 MRCLPVFVILLLTASGPSPYDARLTKTDDVPLSSFRDNASTLQRHQDKSVCVCGYKLCFP 60					
Qy	61 C 61					
Db	61 C 61					
RESULT 4					RESULT 5	
ID ABG9517	standard; protein; 62 AA.				ID ABG95604	standard; protein; 62 AA.
XX					XX	
AC ABG9517;					AC ABG95604;	
XX					XX	
DT 17-JAN-2003	(first entry)				DT 17-JAN-2003	(first entry)
DE Conus sp conotoxin-associated protein SEQ ID 229.					DE Conus sp conotoxin-associated protein SEQ ID 358.	
XX					XX	
KW cone snail; analgesic; voltage-gated ion channel modulator;					KW cone snail; analgesic; voltage-gated ion channel modulator;	
KW ligand-gated ion channel modulator; pain-relief.					KW ligand-gated ion channel modulator; pain-relief.	
XX					XX	
OS Conus textile.					OS Conus textile.	
XX					XX	
PD WO200264740-A2.					PD WO200264740-A2.	
XX					XX	
PN WO200264740-A2.					PN WO200264740-A2.	
XX					XX	
PD 22-AUG-2002.					PD 22-AUG-2002.	
XX					XX	
PP 11-FEB-2002; 2002WO-US003887.					PP 11-FEB-2002; 2002WO-US003887.	
XX					XX	
PR 09-FEB-2001; 2001US-0267408P.					PR 09-FEB-2001; 2001US-0267408P.	
XX					XX	
PA (COGN-) COGNETIX INC.					PA (COGN-) COGNETIX INC.	
PA (UTAH ) UNIV UTAH RES FOUND.					PA (UTAH ) UNIV UTAH RES FOUND.	
XX					XX	
PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;					PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;	
PI Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;					PI Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;	
XX					XX	
XX					XX	
DR WPI: 2002-706921/76.					DR WPI: 2002-706921/76.	
XX					XX	
DR N-PSDB; ABX04939.					DR N-PSDB; ABX04939.	
XX					XX	
PS New cone snail conotoxin peptides, useful as a pain reliever for					PS New cone snail conotoxin peptides, useful as a pain reliever for	
PT alleviating pain in an individual suffering from pain or who is about to					PT alleviating pain in an individual suffering from pain or who is about to	
PT be subjected to a pain-causing event, or for treating voltage-gated ion					PT be subjected to a pain-causing event, or for treating voltage-gated ion	
XX					XX	
CC This invention describes novel conotoxin peptides from the cone snail,					CC This invention describes novel conotoxin peptides from the cone snail,	
CC genus Conus which have analgesic activity and can act as a voltage-gated					CC genus Conus which have analgesic activity and can act as a voltage-gated	
CC ion channel modulator or a ligand-gated ion channel modulator. The					CC ion channel modulator or a ligand-gated ion channel modulator. The	
CC conotoxin peptide is useful as a pain-relieving agent for alleviating					CC conotoxin peptide is useful as a pain-relieving agent for alleviating	
CC pain in an individual who is either exhibiting pain or is about to be					CC pain in an individual who is either exhibiting pain or is about to be	
CC subjected to a pain-causing event. The conotoxin peptide is also useful					CC subjected to a pain-causing event. The conotoxin peptide is also useful	
CC for treating or preventing disorders associated with voltage-gated ion					CC for treating or preventing disorders associated with voltage-gated ion	
CC channel disorders, ligand-gated ion channel disorders or receptor					CC channel disorders, ligand-gated ion channel disorders or receptor	
CC disorders. The radiolabeled conotoxin peptide is also useful for					CC disorders. The radiolabeled conotoxin peptide is also useful for	
CC characterising a new site on these receptors or channels, and for					CC characterising a new site on these receptors or channels, and for	
CC screening and identifying novel small molecules that interact with the					CC screening and identifying novel small molecules that interact with the	
CC above-mentioned channels or receptors, which are monoamine transporters.					CC above-mentioned channels or receptors, which are monoamine transporters.	
CC ABG99360-ABG99853 represent the conotoxin protein and peptides described					CC ABG99360-ABG99853 represent the conotoxin protein and peptides described	
CC in the disclosure of the invention					CC in the disclosure of the invention	
XX					XX	
SQ Sequence 62 AA;					SQ Sequence 62 AA;	
Query Match 84.9%;	Score 281;	DB 5;	Length 62;	Query Match 84.9%;	Score 281;	DB 5;
Best Local Similarity 82.3%;	Pred. No. 1.4e-28;			Best Local Similarity 82.3%;	Pred. No. 1.e-28;	
Matches 51; Conservative 6; Mismatches 6;	Indels -5;	Gaps 0;	Mismatches 5;	Matches 51; Conservative 6; Mismatches 5;	Indels 0;	Gaps 0;
Db				Db		

Qy 61 CG 62  
Db 61 CG 62

RESULT 6  
ABG9593  
ID ABG9593 standard; protein; 64 AA.

XX ABG9593;  
XX DT 17-JAN-2003 (first entry)  
XX Conus sp conotoxin-associated protein SEQ ID 342.  
XX Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;  
XX ligand-gated ion channel modulator; pain-relief.  
OS Conus episcopatus.  
XX PN WO200264740-A2.  
XX PD 22-AUG-2002.  
XX PF 11-FEB-2002; 2002WO-US003887.  
XX PR 09-FEB-2001; 2001US-0267408P.  
XX PA (COGN-) COGNETIX INC.  
PA (UTAH ) UNIV UTAH RES FOUND.  
XX PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;  
PI Grillely M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;  
XX DR WPI; 2002-706921/76.  
XX DR N-PSDB; ABX04940.

New cone snail conotoxin peptides, useful as a pain reliever for  
PT alleviating pain in an individual suffering from pain or who is about to  
PT be subjected to a pain-causing event, or for treating voltage-gated ion  
PT channel disorders.

Claim 1; Page 235; 305pp; English.

This invention describes novel conotoxin peptides from the cone snail,  
genus Conus which have analgesic activity and can act as a voltage-gated  
ion channel modulator or a ligand-gated ion channel modulator. The  
conotoxin peptide is useful as a pain-relieving agent for alleviating  
pain in an individual who is either exhibiting pain or is about to be  
subjected to a pain-causing event. The conotoxin peptide is also useful  
for treating or preventing disorders associated with voltage-gated ion  
channel disorders, ligand-gated ion channel disorders or receptor  
disorders. The radiolabelled conotoxin peptide is also useful for  
characterising a new site on these receptors or channels, and for  
screening and identifying novel small molecules that interact with the  
above-mentioned channels or receptors, which are monoamine transporters.  
ABG9593-ABG9853 represent the conotoxin protein and peptides described  
in the disclosure of the invention

XX Sequence 64 AA;

Query Match Score 272; DB 5; Length 64;  
Best Local Similarity 82.2%; Pred. No. 2.2e-21; Indels 2; Gaps 1;  
Matches 53; Conservative 3; Mismatches 3; Gaps 0;

Qy 1 MRCLPVFVILLITASGPSVDAKSTLQRHQDKSVCCGYKLC 58  
Db 1 MRCLPVFVILLITASGPSVDAKSTLQRHQDKSVCCGYKLC 58

Qy 61 CG 62  
Db 61 CG 62

RESULT 8  
ABG9940  
ID ABG9940 standard; protein; 64 AA.

XX DE Conus sp conotoxin-associated protein SEQ ID 361.  
XX KW Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;  
KW ligand-gated ion channel modulator; pain-relief.  
XX OS Conus ammiralis.  
XX PN WO200264740-A2.  
XX PD 22-AUG-2002.  
XX PF 11-FEB-2002; 2002WO-US003887.  
XX PR 09-FEB-2001; 2001US-0267408P.  
XX PA (COGN-) COGNETIX INC.  
PA (UTAH ) UNIV UTAH RES FOUND.  
XX PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;  
PI Grillely M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;  
XX DR WPI; 2002-706921/76.  
XX DR N-PSDB; ABX04940.

New cone snail conotoxin peptides, useful as a pain reliever for  
PT alleviating pain in an individual suffering from pain or who is about to  
PT be subjected to a pain-causing event, or for treating voltage-gated ion  
PT channel disorders.

Claim 1; Page 241; 305pp; English.

This invention describes novel conotoxin peptides from the cone snail,  
genus Conus which have analgesic activity and can act as a voltage-gated  
ion channel modulator or a ligand-gated ion channel modulator. The  
conotoxin peptide is useful as a pain-relieving agent for alleviating  
pain in an individual who is either exhibiting pain or is about to be  
subjected to a pain-causing event. The conotoxin peptide is also useful  
for treating or preventing disorders associated with voltage-gated ion  
channel disorders, ligand-gated ion channel disorders or receptor  
disorders. The radiolabelled conotoxin peptide is also useful for  
characterising a new site on these receptors or channels, and for  
screening and identifying novel small molecules that interact with the  
above-mentioned channels or receptors, which are monoamine transporters.  
ABG9593-ABG9853 represent the conotoxin protein and peptides described  
in the disclosure of the invention

XX Sequence 62 AA;

Query Match Score 266; DB 5; Length 62;  
Best Local Similarity 82.3%; Pred. No. 1.2e-26;  
Matches 51; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MRCLPVFVILLITASGPSVDAKSTLQRHQDKSVCCGYKLCFP 60  
Db 1 MHLPVVFVILLITASGPSVDAKSTLQRHQDKSVCCGYKLCFP 60

Qy 61 CG 62  
Db 61 CG 62



KW ligand-gated ion channel modulator; pain-relief.  
 OS *Conus pennaceus*.  
 XX WO200264740-A2.  
 PN WO200264740-A2.  
 XX PD 22-AUG-2002.  
 XX PR 09-FEB-2002; 2002WO-US003887.  
 XX PF 11-FEB-2002; 2002WO-US003887.  
 XX PR 09-FEB-2001; 2001US-0267408P.  
 XX PA (COGN-) COGNETIX INC.  
 (UTAH ) UNIV UTAH RES FOUND.  
 PA (COGN-) COGNETIX INC.  
 (UTAH ) UNIV UTAH RES FOUND.  
 PI Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;  
 PI Griley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;  
 XX WPI; 2002-706921/76.  
 DR N-PSDB; ABX04918.  
 XX New cone snail conotoxin peptides, useful as a pain reliever for  
 PT alleviating pain in an individual suffering from pain or who is about to  
 PT be subjected to a pain-causing event, or for treating voltage-gated ion  
 PT channel disorders.  
 XX Claim 1; Page 218; 305pp; English.  
 XX This invention describes novel conotoxin peptides from the cone snail,  
 CC *Conus* which have analgesic activity and can act as a voltage-gated  
 CC channel modulator or a ligand-gated ion channel modulator. The  
 CC conotoxin peptide is useful as a pain-relieving agent for alleviating  
 CC pain in an individual who is either exhibiting pain or is about to be  
 CC subjected to a pain-causing event. The conotoxin peptide is also useful  
 CC for treating or preventing disorders associated with voltage-gated ion  
 CC channel disorders, ligand-gated ion channel disorders or receptor  
 CC disorders. The radiolabelled conotoxin peptide is also useful for  
 CC characterising new site on these receptors or channels, and for  
 CC screening and identifying novel small molecules that interact with the  
 CC above-mentioned channels or receptors, which are monoamine transporters.  
 CC ABG9360-ABC99853 represent the conotoxin protein and peptides described  
 CC in the disclosure of the invention  
 XX Sequence 64 AA;  
 PS Claim 1; Page 242; 305pp; English.  
 XX This invention describes novel conotoxin peptides from the cone snail,  
 CC *Conus* which have analgesic activity and can act as a voltage-gated  
 CC ion channel modulator or a ligand-gated ion channel modulator. The  
 CC conotoxin peptide is useful as a pain-relieving agent for alleviating  
 CC pain in an individual who is either exhibiting pain or is about to be  
 CC subjected to a pain-causing event. The conotoxin peptide is also useful  
 CC for treating or preventing disorders associated with voltage-gated ion  
 CC channel disorders, ligand-gated ion channel disorders or receptor  
 CC disorders. The radiolabelled conotoxin peptide is also useful for  
 CC characterising a new site on these receptors or channels, and for  
 CC screening and identifying novel small molecules that interact with the  
 CC above-mentioned channels or receptors, which are monoamine transporters.  
 CC ABG9360-ABC99853 represent the conotoxin protein and peptides described  
 CC in the disclosure of the invention  
 XX Sequence 64 AA;  
 PS Query Match 79.8%; Score 264; DB 5; Length 64;  
 Best Local Similarity 82.5%; Pred. No. 2.3e-6;  
 Matches 52; Conservative 3; Mismatches 6; Indels 2; Gaps 1;  
 DB 1 MRCLPVFVILLTASGPVDAR-LKTKDDVPLSSFRDNAAKSTLQRHQDKSVC CGYKLCFP 58  
 AC 1 MRCLPVFVILLTASGPVDAR-LKTKDDVPLSSFRDNAAKSTLQRHQDKSVC CGYKLCFP 60  
 AC 1 MRCLPVFVILLTASAPSVDAKVHLKTKDGPLSSFRDNAAKSTLQRHQDKSVC CGYKMC 60  
 AC 59 FPC 61  
 DB 61 IPC 63  
 RESULT 11  
 ABG99611  
 ID ABG99611 standard; protein; 61 AA.  
 XX DT 17-JAN-2003 (first entry)  
 XX AC ABG99611;  
 XX DB Conus sp conotoxin-associated protein SEQ ID 294.  
 KW Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;  
 KW ligand-gated ion channel modulator; pain-relief.  
 OS Conus omaria.  
 XX PN WO200264740-A2.  
 XX PD 22-AUG-2002.  
 XX Query Match 76.9%; Score 254.5; DB 5; Length 61;  
 Best Local Similarity 85.2%; Pred. No. 3.7e-25;  
 Matches 52; Conservative 1; Mismatches 7; Indels 1; Gaps 1;  
 DB 1 MRCLPVFVILLTASGPVDAR-LKTKDDVPLSSFRDNAAKSTLQRHQDKSVC CGYKLCFP 60  
 AC 1 MRCLPVFVILLTASAPSVDAR-LKTKDDVPLSSFRDNAAKSTLQRHQDKSVC CGYKCF-PC 59  
 AC 61 C 61  
 DB 60 C 60  
 RESULT 12  
 ABG99612  
 ID ABG99612 standard; protein; 61 AA.  
 XX AC ABG99612;  
 XX DT 17-JAN-2003 (first entry)  
 XX AC ABG99612;  
 XX DB Conus sp conotoxin-associated protein SEQ ID 370.  
 KW Conotoxin; core snail; analgesic; voltage-gated ion channel modulator;  
 KW ligand-gated ion channel modulator; pain-relief.  
 OS Conus omaria.



PI Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;  
 XX WPI; 2002-706921/76.  
 DR N-PSDB; ABX04847.

XX New cone snail conotoxin peptides, useful as a pain reliever for alleviating pain in an individual suffering from pain or who is about to be subjected to a pain-causing event, or for treating voltage-gated ion channel disorders.

XX Claim 1; Page 130; 305pp; English.

PS This invention describes novel conotoxin peptides from the cone snail, genus Conus which have analgesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders, ligand-gated ion channel disorders or receptor disorders. The radiolabelled conotoxin peptide is also useful for characterising a new site on these receptors or channels, and for screening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters. ABG9360-ABG9353 represent the conotoxin protein and peptides described in the disclosure of the invention

CC Sequence 61 AA;

Query Match 65.3%; Score 216; DB 5; Length 61;  
 Best Local Similarity 68.9%; Pred. No. 3.6e-20;  
 Matches 42; Conservative 3; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MRCLPVFVILLITASGPSPYDARLTKDVPYSSFRDNASTLQRHQDKSVCGGYKLCPFP 60  
 Db 1 MRCLPVLFVILLITASGPSPYDARLTKDVPYSSFRDNASTLQRHQDKSVCGGYKLCPFP 60

Qy 61 C 61  
 Db 61 C 61

Search completed: August 10, 2004, 16:02:37  
 Job time : 81.4324 SECs

---

RESULT 15  
 ABG99598 standard: Protein: 61 AA.  
 ID ABG99598

XX AC ABG99598;  
 XX DT 17-JAN-2003 (first entry)

DE Conus sp conotoxin-associated protein SEQ ID 349.

XX Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;  
 KW ligand-gated ion channel modulator; pain-relief.

XX OS Conus bandanus.

XX PN WO200264740-A2.  
 XX PR 09-FEB-2001; 2001US-0267408P.  
 XX PD 22-AUG-2002.  
 XX PP 11-FEB-2002; 2002WO-US003887.

XX PR 09-FEB-2001; 2001US-0267408P.  
 XX PA (COGN-) COGNETIX INC.  
 PA (UTAH ) UNIV UTAH RES FOUND.  
 XX PI Oliveira BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;  
 PI Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;  
 XX DR WPI; 2002-706921/76.  
 DR N-PSDB; ABX04936.

Result No.	Score	Query Match	Length	DB ID	Description	Sequence
1	206	62.2	59	4	US-09-497-491-37	Sequence 37, App1
2	199	60.1	60	4	US-09-497-491-39	Sequence 39, App1
3	199	60.1	70	4	US-09-497-491-35	Sequence 35, App1
4	180.5	54.5	62	4	US-09-497-491-49	Sequence 49, App1
5	179	54.1	63	4	US-09-497-491-43	Sequence 43, App1
6	169.5	51.2	62	4	US-09-497-491-21	Sequence 21, App1
7	169	51.1	62	4	US-09-497-491-25	Sequence 25, App1
8	167.5	50.6	64	4	US-09-497-491-41	Sequence 41, App1
9	167	50.5	67	4	US-09-497-491-31	Sequence 31, App1
10	166	50.2	67	4	US-09-497-491-33	Sequence 33, App1
11	164	49.5	62	4	US-09-497-491-45	Sequence 45, App1
12	151.5	45.8	61	4	US-09-497-491-23	Sequence 23, App1
13	151.5	45.8	61	4	US-09-497-491-29	Sequence 29, App1
14	148	44.7	63	4	US-09-497-491-47	Sequence 47, App1
15	129.5	39.1	62	4	US-09-497-491-27	Sequence 27, App1
16	59	17.8	111	1	US-08-456-265A-111	Sequence 111, App1
17	59	17.8	111	2	US-08-497-217-111	Sequence 111, App1
18	59	17.8	111	3	US-09-350-600-111	Sequence 111, App1
19	59	17.8	111	4	US-09-497-234-111	Sequence 111, App1
20	57	17.2	216	4	US-09-489-039A-11172	Sequence 11172, A
21	55.5	16.8	312	4	US-09-489-039A-11138	Sequence 11138, A
22	55.5	16.8	423	2	US-08-390-731C-111	Sequence 111, App1
23	55.5	16.8	953	4	US-09-099-041A-8	Sequence 8, App1
24	55.5	16.8	953	4	US-09-245-281-8	Sequence 8, App1
25	55.5	16.8	953	4	US-09-207-359B-8	Sequence 8, App1
26	55.5	16.8	953	4	US-09-340-620A-8	Sequence 8, App1
27	55.5	16.8	953	4	US-09-865-364-8	Sequence 8, App1



LENGTH: 62  
 ; ORGANISM: *Conus textile*  
 US-09-497-491-21

Query Match Score 169; DB 4; Length 62;  
 Best Local Similarity 51.2%; Pred. No. 3e-15;  
 Matches 37; Conservative 5; Mismatches 15; Indels 1; Gaps 1;

Qy 1 MRCLPVFVILLLTASGPSYDARLTKDDVPLSSFRDNASTLQRHDKSVCCTGYKLC 57  
 Db 1 MCCLPVFVILLLTASAPSVDQPKTKDDVPLAQLHDNAKSALQ-HLNQRCQTYWYC 58

RESULT 9  
 US-09-497-491-31  
 ; Sequence 31, Application US/09497491  
 ; Patent No. 6630573  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Walker, Craig  
 ; APPLICANT: Shetty, Reshma  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: Hooper, David  
 ; APPLICANT: Jacobsen, Richard  
 ; APPLICANT: Steele, Doug  
 ; APPLICANT: Jones, Robert M.  
 ; TITLE OF INVENTION: Tau-Conotoxin Peptides  
 ; FILE REFERENCE: Tau-Conopeptides  
 ; CURRENT APPLICATION NUMBER: US/09/497,491  
 ; CURRENT FILING DATE: 2000-02-04  
 ; EARLIER APPLICATION NUMBER: US 60/118,642  
 ; EARLIER FILING DATE: 1999-02-04  
 ; NUMBER OF SEQ ID NOS: 49  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 31  
 ; LENGTH: 67  
 ; TYPE: PRT  
 ; ORGANISM: *Conus textile*  
 US-09-497-491-31

Query Match Score 167; DB 4; Length 67;  
 Best Local Similarity 50.6%; Pred. No. 5.7e-15;  
 Matches 35; Conservative 6; Mismatches 1; Indels 1; Gaps 1;

Qy 1 MRCLPVFVILLLTASGPSYDARLTKDDVPLSSFRDNASTLQRHDKSVCCTGYKRL 57  
 Db 1 MRCLPVFVILLLTASAPSVDQPKTKDDVPLAQLHDNAKSALQ-HLNQRCQTYWXR-CCPRL 56

RESULT 9  
 US-09-497-491-31  
 ; Sequence 31, Application US/09497491  
 ; Patent No. 6630573  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Walker, Craig  
 ; APPLICANT: Shetty, Reshma  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: Hooper, David  
 ; APPLICANT: Jacobsen, Richard  
 ; APPLICANT: Steele, Doug  
 ; APPLICANT: Jones, Robert M.  
 ; TITLE OF INVENTION: Tau-Conotoxin Peptides  
 ; FILE REFERENCE: Tau-Conopeptides  
 ; CURRENT APPLICATION NUMBER: US/09/497,491  
 ; CURRENT FILING DATE: 2000-02-04  
 ; EARLIER APPLICATION NUMBER: US 60/118,642  
 ; EARLIER FILING DATE: 1999-02-04  
 ; NUMBER OF SEQ ID NOS: 49  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 31  
 ; LENGTH: 67  
 ; TYPE: PRT  
 ; ORGANISM: *Conus textile*  
 US-09-497-491-31

Query Match Score 167; DB 4; Length 67;  
 Best Local Similarity 62.3%; Pred. No. 7.1e-15;  
 Matches 33; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRCLPVFVILLLTASGPSYDARLTKDDVPLSSFRDNASTLQRHDKSVCCTGYKLC 53  
 Db 1 MRCPVFVILLLTASAPSVDQPKTKDDVPLSSLRDLNKLRTIRLNLRECC 53

RESULT 10  
 US-09-497-491-33  
 ; Sequence 33, Application US/09497491  
 ; Patent No. 6630573  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Walker, Craig  
 ; APPLICANT: Shetty, Reshma  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: Hooper, David  
 ; APPLICANT: Jacobsen, Richard  
 ; APPLICANT: Steele, Doug  
 ; APPLICANT: Jones, Robert M.  
 ; TITLE OF INVENTION: Tau-Conotoxin Peptides  
 ; FILE REFERENCE: Tau-Conopeptides  
 ; CURRENT APPLICATION NUMBER: US/09/497,491  
 ; CURRENT FILING DATE: 2000-02-04  
 ; EARLIER APPLICATION NUMBER: US 60/118,642  
 ; EARLIER FILING DATE: 1999-02-04  
 ; NUMBER OF SEQ ID NOS: 49  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 33  
 ; LENGTH: 67  
 ; TYPE: PRT  
 ; ORGANISM: *Conus textile*  
 US-09-497-491-33

Query Match Score 166; DB 4; Length 67;

Best Local Similarity 62.3%; Pred. No. 9.6e-15; Indels 0; Gaps 0;  
 Matches 33; Conservative 4; Mismatches 16;

Qy 1 MRCLPVFVILLLTASCPVDARLTKTDDVPLSSFRD-NAKSTLQRHQ---DKSVCC 53  
 Db 1 MCCLPVFVILLLTAPSVDALPKTRDDVPLASFGGYNARRILQRQGMCKENIACC 60

RESULT 13  
 US-09-497-491-29  
 ; Sequence 29, Application US/09497491  
 ; Patent No. 6630573  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Walker, Craig  
 ; APPLICANT: Shetty, Reshma  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: Hooper, David  
 ; APPLICANT: Jacobsen, Richard  
 ; APPLICANT: Steele, Doug M.  
 ; TITLE OF INVENTION: Tau-Conotoxin Peptides  
 ; FILE REFERENCE: Tau-Conopeptides  
 ; CURRENT APPLICATION NUMBER: US/09/497,491  
 ; CURRENT FILING DATE: 2000-02-04  
 ; EARLIER APPLICATION NUMBER: US 60/118,642  
 ; EARLIER FILING DATE: 1999-02-04  
 ; NUMBER OF SEQ ID NOS: 49  
 ; SEQ ID NO 29  
 ; LENGTH: 61  
 ; TYPE: PRT  
 ; ORGANISM: Conus geographus  
 US-09-497-491-29

Query Match 45.8%; Score 151.5; DB 4; Length 61;  
 Best Local Similarity 58.3%; Pred. No. 7e-13; Indels 7; Gaps 2;  
 Matches 35; Conservative 4; Mismatches 14;

Qy 1 MRCLPVFVILLLTASCPVDARLTKTDDVPLSSFRD-NAKSTLQRHQ---DKSVCC 53  
 Db 1 MCCLPVFVILLLTAPSVDALPKTRDDVPLASFGGYNARRILQRQGMCKENIACC 60

RESULT 14  
 US-09-497-491-47  
 ; Sequence 47, Application US/09497491  
 ; Patent No. 6630573  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Walker, Craig  
 ; APPLICANT: Shetty, Reshma  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: Hooper, David  
 ; APPLICANT: Jacobsen, Richard  
 ; APPLICANT: Steele, Doug M.  
 ; TITLE OF INVENTION: Tau-Conotoxin Peptides  
 ; FILE REFERENCE: Tau-Conopeptides  
 ; CURRENT APPLICATION NUMBER: US/09/497,491  
 ; CURRENT FILING DATE: 2000-02-04  
 ; EARLIER APPLICATION NUMBER: US 60/118,642  
 ; EARLIER FILING DATE: 1999-02-04  
 ; NUMBER OF SEQ ID NOS: 49  
 ; SEQ ID NO 47  
 ; LENGTH: 63  
 ; TYPE: PRT  
 ; ORGANISM: Conus gloriamaris  
 US-09-497-491-47

Query Match 44.7%; Score 148; DB 4; Length 63;  
 Best Local Similarity 58.5%; Pred. No. 2.1e-12; Indels 0; Gaps 0;  
 Matches 31; Conservative 7; Mismatches 15;

Qy 1 MRCLPVFVILLLTASCPVDARLTKTDDVPLSSFRD-NAKSTLQRHQDKSVCC 53  
 Db 1 MRYLPVFEVILLLTASCPVDARLTKTDDVPLASFGNGRILMSNKRLLC 53

RESULT 12  
 US-09-497-491-23  
 ; Sequence 23, Application US/09497491  
 ; Patent No. 6630573  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Walker, Craig  
 ; APPLICANT: Shetty, Reshma  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: Hooper, David  
 ; APPLICANT: Jacobsen, Richard  
 ; APPLICANT: Steele, Doug M.  
 ; TITLE OF INVENTION: Tau-Conotoxin Peptides  
 ; FILE REFERENCE: Tau-Conopeptides  
 ; CURRENT APPLICATION NUMBER: US/09/497,491  
 ; CURRENT FILING DATE: 2000-02-04  
 ; EARLIER APPLICATION NUMBER: US 60/118,642  
 ; EARLIER FILING DATE: 1999-02-04  
 ; NUMBER OF SEQ ID NOS: 49  
 ; SEQ ID NO 23  
 ; LENGTH: 61  
 ; TYPE: PRT  
 ; ORGANISM: Conus geographus  
 US-09-497-491-23

Query Match 45.8%; Score 151.5; DB 4; Length 61;  
 Best Local Similarity 58.3%; Pred. No. 7e-13; Indels 7; Gaps 2;

RESULT 15  
US-09-497-491-27  
Sequence 27, Application US/09497491  
Patent No. 6630573  
GENERAL INFORMATION:  
APPLICANT: Walker, Craig  
APPLICANT: Shetty, Reshma  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Hooper, David  
APPLICANT: Jacobsen, Richard  
APPLICANT: Steele, Doug  
APPLICANT: Jones, Robert M.  
TITLE OF INVENTION: Tau-Conotoxin Peptides  
FILE REFERENCE: Tau-Conopeptides  
CURRENT APPLICATION NUMBER: US/09/497,491  
CURRENT FILING DATE: 2000-03-04  
EARLIER APPLICATION NUMBER: US 60/118,642  
EARLIER FILING DATE: 1999-02-04  
NUMBER OF SEQ ID NOS: 49  
SEQ ID NO: 27  
LENGTH: 62  
TYPE: PRT  
ORGANISM: Conus imperialis  
US-09-497-491-27

Query Match Score 129.5; DB 4; Length 62;  
Best Local Similarity 50.8%; Pred. No. 5.8e-10;  
Matches 32; Conservative 5; Mismatches 23; Indels 3; Gaps 2;  
Qy 1 MRCLPVFVILLTATGSPYDARLTKDDYPLSSPRDNAKSTLQRHDKSYCCGYKL-CF 59  
Db 1 MYCLPVFVILLIILISSAPSITPPQPRNKDRRLISLLDNDHKGILQR-DWNSCCGRNPGCC 58  
Qy 60 PCG 62  
Db 59 PWG 61

Search completed: August 10, 2004, 16:05:36  
Job time : 25.2973 secs

Billie Sneed

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compagen Ltd.

OM protein - protein search, using sw model

Run on: August 10, 2004, 16:04:26 ; Search time 67.8649 Seconds  
Perfect score: 286.575 Million cell updates/sec

Title: US-10-072-602B-352

Sequence: 1 MRCLPVFVILLIITASGPSPV.....LQRHQDKSVCCGGYKLCFP CG 62

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 1291235 seqs, 313682936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Database : Published Applications AA:  
 1: /cgn2\_6/\_ptodata/2/\_pubpaa/\_us07\_PUBCOMB.pep:  
 2: /cgn2\_6/\_ptodata/2/\_pubpaa/\_us08\_PUBCOMB.pep:  
 3: /cgn2\_6/\_ptodata/2/\_pubpaa/\_us06\_NEW\_PUB.pep:  
 4: /cgn2\_6/\_ptodata/2/\_pubpaa/\_us05\_PUBCOMB.pep:  
 5: /cgn2\_6/\_ptodata/2/\_pubpaa/\_us07\_NEW\_PUB.pep:  
 6: /cgn2\_6/\_ptodata/2/\_pubpaa/\_us05\_PUBCOMB.pep:  
 7: /cgn2\_6/\_ptodata/2/\_pubpaa/\_us08\_NEW\_PUB.pep:  
 8: /cgn2\_6/\_ptodata/2/\_pubpaa/\_us09\_PUBCOMB.pep:  
 9: /cgn2\_6/\_ptodata/2/\_pubpaa/\_us09a\_PUBCOMB.pep:  
 10: /cgn2\_6/\_ptodata/2/\_pubpaa/\_us09b\_PUBCOMB.pep:  
 11: /cgn2\_6/\_ptodata/2/\_pubpaa/\_us09c\_PUBCOMB.pep:  
 12: /cgn2\_6/\_ptodata/2/\_pubpaa/\_us09\_NEW\_PUB.pep:  
 13: /cgn2\_6/\_ptodata/2/\_pubpaa/\_us10a\_PUBCOMB.pep:  
 14: /cgn2\_6/\_ptodata/2/\_pubpaa/\_us10b\_PUBCOMB.pep:  
 15: /cgn2\_6/\_ptodata/2/\_pubpaa/\_us10c\_PUBCOMB.pep:  
 16: /cgn2\_6/\_ptodata/2/\_pubpaa/\_us10\_NEW\_PUB.pep:  
 17: /cgn2\_6/\_ptodata/2/\_pubpaa/\_us60\_NEW\_PUBCOMB.pep:  
 18: /cgn2\_6/\_ptodata/2/\_pubpaa/\_us60\_PUBCOMB.pep:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	%		
1	331	100.0	62	14	US-10-072-602B-152	Sequence 352, App	Score 331; DB 14;	Length 62;
2	298	90.0	62	14	US-10-072-602B-339	Sequence 339, App	Score 100%; Pre. No. 3.1e-33;	Gaps 0;
3	286	86.4	62	14	US-10-072-602B-336	Sequence 336, App	Number of SEQ ID NOS: 638	
4	281	84.9	62	14	US-10-072-602B-229	Sequence 229, App	Prior Application Number: US-10-072-602B-330	
5	281	84.9	62	14	US-10-072-602B-358	Sequence 358, App	Software: Patentin version 3.0	
6	276	83.4	64	14	US-10-072-602B-342	Sequence 342, App	SEQ ID NO: 352	
7	266	80.4	62	14	US-10-072-602B-361	Sequence 361, App	Length: 62	
8	264	79.8	64	14	US-10-072-602B-162	Sequence 162, App	Type: PRT	
9	264	79.8	64	14	US-10-072-602B-333	Sequence 333, App	Organism: Conus aulicus	
10	264	79.8	64	14	US-10-072-602B-364	Sequence 364, App	US-10-072-602B-352	
11	254.5	76.9	61	14	US-10-072-602B-294	Sequence 294, App	Query Match 100.0%; Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;	
12	253.5	76.6	61	14	US-10-072-602B-370	Sequence 370, App	1 MRCLPVFVILLITASGPSPVDAKLTQDPLSSFRDNAKSTLQRHQDKSVC CGYKLCP 60	
13	220	66.5	60	14	US-10-072-602B-306	Sequence 306, App	1 MRCLPVFVILLITASGPSPVDAKLTQDPLSSFRDNAKSTLQRHQDKSVC CGYKLCP 60	
14	216	65.3	61	14	US-10-072-602B-62	Sequence 62, App		
15	216	65.3	61	14	US-10-072-602B-349	Sequence 349, App		

RESULT 2  
 US-10-072-602B-339  
 ; Sequence 339, Application US/10072602B  
 ; Publication No. US20030109670A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Utah Research Foundation  
 ; INVENTION: Cone Snail Peptides  
 ; FILE REFERENCE: 2314-249  
 ; CURRENT APPLICATION NUMBER: US 10/072,602B  
 ; CURRENT FILING DATE: 2002-02-11  
 ; PRIOR APPLICATION NUMBER: US 60/267,408  
 ; PRIOR FILING DATE: 2001-02-09  
 ; NUMBER OF SEQ ID NOS: 638  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 339  
 ; LENGTH: 62  
 ; TYPE: PRT  
 ; ORGANISM: Conus pennaceus  
 ; US-10-072-602B-339

Query Match 90.0%; Score 298; DB 14; Length 62;  
 Best Local Similarity 88.7%; Pred. No. 3; Mismatches 4; Indels 0; Gaps 0;  
 Matches 55; Conservative 5; MisMatches 4; Del 0; Gap 0;

Qy 1 MRCLPYFVILLTATSGPSVDARLTKTDVPLSSFRDNAKSTLQRHODKSVCYCGYLICFP 60  
 Db 1 MRCLPYFVILLTATSGPSVDARLTKTDVPLSSFRDNAKSTLQRHODKSVCYCGYLICFP 60

Qy 61 CG 62  
 Db 61 CG 62

RESULT 3  
 US-10-072-602B-336  
 ; Sequence 336, Application US/10072602B  
 ; Publication No. US20030109670A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Utah Research Foundation  
 ; INVENTION: Cone Snail Peptides  
 ; FILE REFERENCE: 2314-249  
 ; CURRENT APPLICATION NUMBER: US 10/072,602B  
 ; CURRENT FILING DATE: 2002-02-11  
 ; PRIOR APPLICATION NUMBER: US 60/267,408  
 ; PRIOR FILING DATE: 2001-02-09  
 ; NUMBER OF SEQ ID NOS: 638  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 229  
 ; LENGTH: 62  
 ; TYPE: PRT  
 ; ORGANISM: Conus textile  
 ; US-10-072-602B-336

Query Match 84.9%; Score 281; DB 14; Length 62;  
 Best Local Similarity 82.3%; Pred. No. 4; Mismatches 6; Indels 5; Gaps 0;  
 Matches 51; Conservative 6; MisMatches 6; Del 5; Gap 0;

Qy 1 MRCLPYFVILLTATSGPSVDARLTKTDVPLSSFRDNAKSTLQRHODKSVCYCGYLICFP 60  
 Db 1 MHCLPYFVILLTATSGPSVDARLTKTDVPLSSFRDNAKSTLQRHODKSVCYCGYLICFP 60

Qy 61 CG 62  
 Db 61 CG 62

RESULT 4  
 US-10-072-602B-229  
 ; Sequence 229, Application US/10072602B  
 ; Publication No. US20030109670A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Utah Research Foundation  
 ; INVENTION: Cone Snail Peptides  
 ; FILE REFERENCE: 2314-249  
 ; CURRENT APPLICATION NUMBER: US 10/072,602B  
 ; CURRENT FILING DATE: 2002-02-11  
 ; PRIOR APPLICATION NUMBER: US 60/267,408  
 ; PRIOR FILING DATE: 2001-02-09  
 ; NUMBER OF SEQ ID NOS: 638  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 229  
 ; LENGTH: 62  
 ; TYPE: PRT  
 ; ORGANISM: Conus textile  
 ; US-10-072-602B-229

Query Match 84.9%; Score 281; DB 14; Length 62;  
 Best Local Similarity 82.3%; Pred. No. 4; Mismatches 6; Indels 5; Gaps 0;  
 Matches 51; Conservative 6; MisMatches 6; Del 5; Gap 0;

Qy 1 MRCLPYFVILLTATSGPSVDARLTKTDVPLSSFRDNAKSTLQRHODKSVCYCGYLICFP 60  
 Db 1 MHCLPYFVILLTATSGPSVDARLTKTDVPLSSFRDNAKSTLQRHODKSVCYCGYLICFP 60

Qy 61 CG 62  
 Db 61 CG 62

RESULT 5  
 US-10-072-602B-358  
 ; Sequence 358, Application US/10072602B  
 ; Publication No. US20030109670A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Utah Research Foundation  
 ; INVENTION: Cone Snail Peptides  
 ; FILE REFERENCE: 2314-249  
 ; CURRENT APPLICATION NUMBER: US 10/072,602B  
 ; CURRENT FILING DATE: 2002-02-11  
 ; PRIOR APPLICATION NUMBER: US 60/267,408  
 ; PRIOR FILING DATE: 2001-02-09  
 ; NUMBER OF SEQ ID NOS: 638  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 358  
 ; LENGTH: 62  
 ; TYPE: PRT  
 ; ORGANISM: Conus textile  
 ; US-10-072-602B-358

Query Match 84.9%; Score 281; DB 14; Length 62;  
 Best Local Similarity 82.3%; Pred. No. 4; Mismatches 6; Indels 5; Gaps 0;  
 Matches 51; Conservative 6; MisMatches 6; Del 5; Gap 0;

Qy 1 MRCLPYFVILLTATSGPSVDARLTKTDVPLSSFRDNAKSTLQRHODKSVCYCGYLICFP 60  
 Db 1 MHCLPYFVILLTATSGPSVDARLTKTDVPLSSFRDNAKSTLQRHODKSVCYCGYLICFP 60

Qy 61 CG 62  
 Db 61 CG 62



PRIOR FILING DATE: 2001-02-09  
 NUMBER OF SEQ ID NOS: 638  
 SOFTWARE: PatentIn version 3.0  
 SEQ ID NO: 162  
 LENGTH: 64  
 TYPE: PRT  
 ORGANISM: Conus pennaceus  
 US-10-072-602B-162

Query Match 99.8%; Score 264; DB 14; Length 64;  
 Best Local Similarity 82.5%; Pred. No. 6e-25; Indels 2; Gaps 1;  
 Matches 52; Conservative 3; Mismatches 6;

Qy 1 MRCLPVFVILLTATGSPVDAR-LKTKDDVPSSFRDNAKSTLQRHODKSVCVCGYKLC 58  
 Db 1 MRCLPVFVILLTATGSPVDAR-LKTKDDVPSSFRDNAKSTLQRHODKSVCVCGYKLC 60

Qy 59 FPC 61  
 Db 61 IPC 63

---

RESULT 9  
 US-10-072-602B-333  
 ; Sequence 333, Application US/10072602B  
 ; Publication No. US20030109670A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Utah Research Foundation  
 ; APPLICANT: Cognetix, Inc.  
 ; APPLICANT: Oliver, Baldomero M.  
 ; APPLICANT: McIntosh, J., Michael  
 ; APPLICANT: Watkins, Maren  
 ; APPLICANT: Garrett, James E.  
 ; APPLICANT: Cruz, Lourdes J.  
 ; APPLICANT: Grille, Michelle  
 ; APPLICANT: Schoenfeld, Robert M.  
 ; APPLICANT: Walker, Craig  
 ; APPLICANT: Shetty, Reshma  
 ; APPLICANT: Jones, Robert M.  
 ; TITLE OF INVENTION: Cone Snail Peptides  
 ; FILE REFERENCE: 2314-249  
 ; CURRENT APPLICATION NUMBER: US/10/072,602B  
 ; CURRENT FILING DATE: 2002-02-11  
 ; PRIOR APPLICATION NUMBER: US 60/267,408  
 ; PRIOR FILING DATE: 2001-02-09  
 ; NUMBER OF SEQ ID NOS: 638  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 333  
 ; LENGTH: 64  
 ; TYPE: PRT  
 ; ORGANISM: Conus pennaceus  
 US-10-072-602B-333

Query Match 99.8%; Score 264; DB 14; Length 64;  
 Best Local Similarity 82.5%; Pred. No. 6e-25; Indels 2; Gaps 1;  
 Matches 52; Conservative 3; Mismatches 6;

Qy 1 MRCLPVFVILLTATGSPVDAR-LKTKDDVPSSFRDNAKSTLQRHODKSVCVCGYKLC 58  
 Db 1 MRCLPVFVILLTATGSPVDAR-LKTKDDVPSSFRDNAKSTLQRHODKSVCVCGYKLC 60

Qy 59 FPC 61  
 Db 61 IPC 63

---

RESULT 10  
 US-10-072-602B-364  
 ; Sequence 364, Application US/10072602B  
 ; Publication No. US20030109670A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Utah Research Foundation  
 ; APPLICANT: Cognetix, Inc.

RESULT 12  
 US-10-072-602B-370  
 ; Sequence 370, Application US/10/072602B  
 ; Publication No. US20030109670A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Utah Research Foundation  
 ; Cognetix, Inc.  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: McIntosh, J., Michael  
 ; APPLICANT: Watkins, Maren  
 ; APPLICANT: Garrett, James E.  
 ; APPLICANT: Cruz, Lourdes J.  
 ; APPLICANT: Grilley, Michelle  
 ; APPLICANT: Schoenfeld, Robert M.  
 ; APPLICANT: Walker, Craig  
 ; APPLICANT: Shetty, Reshma  
 ; TITLE OF INVENTION: Cone Snail Peptides  
 ; FILE REFERENCE: 2314 249  
 ; CURRENT APPLICATION NUMBER: US/10/072, 602B  
 ; FILING DATE: 2002-02-11  
 ; PRIOR APPLICATION NUMBER: US 60/267, 408  
 ; NUMBER OF SEQ ID NOS: 638  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 370  
 ; LENGTH: 61  
 ; TYPE: PRT  
 ; ORGANISM: Conus omaria  
 US-10-072-602B-370

Query Match 76.6%; Score 253.5; DB 14; Length 61;  
 Best Local Similarity 83.6%; Pred. No. 1.e-23;  
 Matches 51; Conservative 2; Mismatches 7; Indels 1; Gaps 1;  
 Qy 1 MRCLPFPVILLILATASGPSSDARPLKDDPLSSFRDNAKSTLQRQHQDKSVCCGYKLCP 60  
 Db 1 MRCLPFPVILLILATASGPSSDARPLKDDPLSSFRDNAKSTLQRQHQDKSVCCYVRMC-P 59

Qy 61 C 61  
 Db 60 C 60

RESULT 13  
 US-10-072-602B-306  
 ; Sequence 306, Application US/10/072602B  
 ; Publication No. US20030109670A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Utah Research Foundation  
 ; Cognetix, Inc.  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: McIntosh, J., Michael  
 ; APPLICANT: Watkins, Maren  
 ; APPLICANT: Garrett, James E.  
 ; APPLICANT: Cruz, Lourdes J.  
 ; APPLICANT: Grilley, Michelle  
 ; APPLICANT: Schoenfeld, Robert M.  
 ; APPLICANT: Walker, Craig  
 ; APPLICANT: Shetty, Reshma  
 ; APPLICANT: Jones, Robert M.  
 ; TITLE OF INVENTION: Cone Snail Peptides  
 ; FILE REFERENCE: 2314 249  
 ; CURRENT APPLICATION NUMBER: US/10/072, 602B  
 ; FILING DATE: 2002-02-11  
 ; PRIOR APPLICATION NUMBER: US 60/267, 408  
 ; NUMBER OF SEQ ID NOS: 638  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 62  
 ; LENGTH: 61  
 ; TYPE: PRT  
 ; ORGANISM: Conus bandanus  
 US-10-072-602B-306

Query Match 65.3%; Score 216; DB 14; Length 61;  
 Best Local Similarity 68.9%; Pred. No. 7.e-19;  
 Matches 42; Conservative 3; Mismatches 16; Indels 0; Gaps 0;  
 Qy 1 MRCLPFPVILLILATASGPSSDARPLKDDPLSSFRDNAKSTLQRQHQDKSVCCGYKLCP 60  
 Db 1 MRCLPFPVILLILATASGPSSDARPLKDDPLSSFRDNAKSTLQRQHQDKSVCCYKLCP 60  
 Qy 61 C 61  
 Db 61 C 61

RESULT 15  
 US-10-072-602B-349  
 ; Sequence 349, Application US/10/072602B  
 ; Publication No. US20030109670A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Utah Research Foundation

```

; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J. Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grillee, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; APPLICANT: Jones, Robert M.

; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIORITY NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 349
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Conus bandanus
; US-10-072-602B-349

Query Match          65.3% ; Score 216; DB 14; Length 61;
Best Local Similarity 68.9%; Pred. No. 4 7e-19;
Matches 42; Conservative 3; Missmatches 16; Indels 0;
Gaps 0;
Qy      1 MRCLPFPVLLILITASGPSVDARLKTIDVPLSSFRDNAAKSTLQRHQDKSVCCGYKLCCFP 60
Db      1 MRCLPFPVLLILITASGPSVDARLKTIDVPLSSFRDNAAKSTLQRHQDKSVCCGYKLCCFP 60
Qy      61 C 61
Db      61 C 61

```

GenCore version 5.1.6  
 Copyright (c) 1993 - 2004 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: August 10, 2004, 16:00:00 ; Search time 19:2703 Seconds  
 (without alignments)  
 309.486 Million cell updates/sec

Title: US-10-072-602B-352

Perfect score: 331

Sequence: MRCLPVFVILLTATSGPSV.....LORHQDKSVCCGYKLCPGCG 62

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched:

283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing First 45 summaries

Database : PIR\_78:\*

1: Piri:\*

2: piri:\*

3: Piri:\*

4: Piri:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	188	56.8	63	2	B59147		conotoxin P5.1 pre
2	180.5	54.5	62	2	B59147		conotoxin Gm5.2 pr
3	169.5	51.2	62	2	B59147		conotoxin Tx5.1 pr
4	167	50.5	67	2	B59147		conotoxin Tx5.2 pr
5	148	44.7	63	2	B59147		conotoxin Gm5.1 pr
6	129.5	39.1	62	2	B59147		conotoxin Im5.1 pr
7	63	19.0	423	2	B89784		hypothetical prote
8	62	18.7	715	2	S77439		hypothetical prote
9	61	18.4	315	1	HNVZVI		hemagglutinin prec
10	60	18.1	389	2	H90413		conserved hypothet
11	59.5	18.0	457	2	T18347		gag protein homolo
12	59	18.0	2148	1	A56081		insulin receptor -
13	59	17.8	111	2	T03701		SAR8.2E protein; T
14	58	17.5	551	2	A11093		oligopeptide ABC t
15	58	17.5	929	2	A32495		rep-1 protein, for
16	58	17.5	1126	2	JC4019		DNA mismatch repair
17	58	17.5	1131	2	T38744		hypothetical prote
18	58	17.5	1992	1	S02771		myosin heavy chain
19	57.5	17.4	1788	2	T48200		hypothetical prote
20	57.5	17.4	541	2	T47290		hypothetical prote
21	57.5	17.4	772	2	HB4605		phosphoribosylamin
22	57.5	17.4	802	1	A26343		hypothetical prote
23	57	17.2	323	2	I64240		outer membrane pro
24	57	17.2	453	2	B99738		fasciclin I precursor
25	57	17.2	662	2	A29900		hypothetical prote
26	56	16.9	369	2	S74983		hypothetical prote
27	56	16.9	633	2	T27499		hypothetical prote
28	56	16.9	975	2	T29908		hypothetical prote
29	55.5	16.8	165	2	H84634		hypothetical prote

Total number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## ALIGNMENTS

## RESULT 1

F59147

conotoxin P5.1 precursor - cone shell (*Conus purpurascens*)

N; Contains: conotoxin p5a

C; Species: *Conus purpurascens* (purple cone)

C; Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 19-May-2000

C; Accession: F59147

R; Walker, C.S.; Steel, D.; Jacobsen, R.B.; Cruz, L.J.; Hooper, D.; Shetty J. Biol. Chem. 274, 30664-30671, 1999

A; Title: The T-supersfamily of conotoxins.

A; Reference number: A59147; PMID:9942558; PMID:10521453

A; Accession: F59147

A; Status: preliminary; not compared with conceptual translation

A; Molecule type: mRNA; protein.

A; Note: submitted to GenBank, July 1999

A; Residues: 1-63 &lt;WAL&gt;

A; Cross-references: GB:AF167168; NID:96103614; PIDN:AAF03688.1; PID:96103615

C; Superfamily: unassigned conotoxins

C; Keywords: amidated carboxyl end; toxin; venom

C; Accession: F59147

C; Status: preliminary; not compared with conceptual translation

A; Note: submitted to GenBank, July 1999

A; Residues: 1-63 &lt;WAL&gt;

A; Cross-references: GB:AF167168; NID:96103614; PIDN:AAF03688.1; PID:96103615

C; Superfamily: unassigned conotoxins

C; Keywords: amidated carboxyl end; toxin; venom

C; Accession: F59147

C; Status: preliminary; not compared with conceptual translation

A; Note: submitted to GenBank, July 1999

A; Residues: 1-63 &lt;WAL&gt;

A; Cross-references: GB:AF167168; NID:96103614; PIDN:AAF03688.1; PID:96103615

C; Superfamily: unassigned conotoxins

C; Keywords: amidated carboxyl end; toxin; venom

C; Accession: F59147

C; Status: preliminary; not compared with conceptual translation

A; Note: submitted to GenBank, July 1999

A; Residues: 1-62 &lt;WAL&gt;

A; Cross-references: GB:AF167168; NID:96103614; PIDN:AAF03688.1; PID:96103615

C; Superfamily: unassigned conotoxins

C; Keywords: amidated carboxyl end; toxin; venom

C; Accession: F59147

C; Status: preliminary; not compared with conceptual translation

A; Note: submitted to GenBank, July 1999

A; Residues: 1-62 &lt;WAL&gt;

A; Cross-references: GB:AF167168; NID:96103614; PIDN:AAF03688.1; PID:96103615

C; Superfamily: unassigned conotoxins

C; Keywords: amidated carboxyl end; toxin; venom

F;1-22/Domain: signal sequence #status predicted <SIG>  
 F;23-49/Domain: propeptide #status predicted <PRO>  
 F;50-60/Product: conotoxin gm5 #status predicted <MAT>  
 F;51-58,52-59/Disulfide bonds: #status predicted  
 F;60/Modified site: amidated carboxyl end (Ser) (amide in mature form from following gly)

Query Match 54.5%; Score 180.5.; DB 2; Length 62;  
 Best Local Similarity 71.7%; Pred. No. 8.5e-15;  
 Matches 38; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

Qy 1 MRCLPVFVILLIITASGPVDARLTKTDDVPLSSFRDNAKSTLQRHDKSVCC 53  
 Db 1 MRCLPVFVILLIITASGPVDARLTKTDDVPLSSFRDNAKSTLQRHDKSVCC 52

RESULT 3  
 B59147 conotoxin Tx5.1 precursor - cone shell (Conus gloriamaris)  
 C;Species: Conus gloriamaris (glory-of-the-sea cone)  
 C;Accession: B59147  
 R;Walker, C.S.; Steel, D.; Jacobsen, R.B.; Lirazan, M.B.; Cruz, L.J.; Hooper, D.; Shetty J.; Biol. Chem., 274, 30664-30671, 1999  
 A;Title: The T<sub>-</sub>superfamily of conotoxins  
 A;Reference number: A59147; MUID:99452958; PMID:10521453  
 A;Accession: B59147  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-62 <WAL>  
 A;Cross-references: GB:AF167164; NID:g6103606; PIDN:AAF03684.1; PID:g6103607  
 A;Note: submitted to GenBank, July 1999  
 C;Keywords: unassigned conotoxins  
 C;Superfamily: amidated carboxyl end; toxin; venom  
 F;1-22/Domain: signal sequence #status predicted <SIG>  
 F;23-49/Domain: propeptide #status predicted <PRO>  
 F;50-60/Product: conotoxin tx5 #status predicted <MAT>  
 F;50-57,51-58/Disulfide bonds: #status predicted  
 F;60/Modified site: amidated carboxyl end (Gln) (amide in mature form from following gly)

Query Match 51.2%; Score 169.5.; DB 2; Length 62;  
 Best Local Similarity 63.8%; Pred. No. 1.8e-13;  
 Matches 37; Conservative 5; Mismatches 15; Indels 1; Gaps 1;

Qy 1 MRCLPVFVILLIITASGPVDARLTKTDDVPLSSFRDNAKSTLQRHDKSVCC 58  
 Db 1 MCCLPVFVILLIITASGPVDARLTKTDDVPLSSFRDNAKSTLQRHDKSVCC 57

RESULT 4  
 B59147 conotoxin Tx5.2 precursor [validated] - cone shell (Conus textile)  
 N;Alternate names: epsilon conotoxin Tx5  
 C;Species: Conus textile (cloth-of-gold cone)  
 C;Dte: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 20-Oct-2000  
 C;Accession: E59147; A59044  
 R;Walker, C.S.; Steel, D.; Jacobsen, R.B.; Lirazan, M.B.; Cruz, L.J.; Hooper, D.; Shetty J.; Biol. Chem., 274, 30664-30671, 1999  
 A;Title: The T<sub>-</sub>superfamily of conotoxins  
 A;Reference number: A59147; MUID:99452958; PMID:10521453  
 A;Accession: E59147  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-67 <WAL>  
 A;Cross-references: GB:AF167167; NID:g6103612; PIDN:AAF03687.1; PID:g6103613  
 A;Note: submitted to GenBank, July 1999; named tx5 in GenBank entry AF167167, release 1  
 R;Rigby, A.C.; Lucas-Meunier, E.; Kalume, D.E.; Czerwiec, E.; Hambe, B.; Dahlqvist, I.; Proc. Natl. Acad. Sci. U.S.A. 96, 5758-5763, 1999  
 A;Title: A conotoxin from Conus textile with unusual posttranslational modifications red  
 A;Reference number: A59044; MUID:99254114; PMID:10318957  
 A;Accession: A59044  
 A;Status: preliminary  
 A;Molecule type: protein

C;Superfamily: unassigned conotoxins  
 C;Keywords: amidated carboxyl end; toxin; venom

A;Residues: 51-63 <RIG>  
 C;Comment: This conotoxin reduces both presynaptic calcium influx and acetylcholine release  
 C;Superfamily: unassigned conotoxins  
 C;Keywords: bromine; carboxyglutamic acid; glycoprotein; hydroxyproline; toxin; venom  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;20-50/Domain: amino-terminal propeptide #status predicted <PRO>  
 F;51-63/Domain: conotoxin tx5 #status experimental <MAT>  
 F;51-54/Domain: carboxy-terminal propeptide #status predicted  
 F;52-58,53-59/Disulfide bonds: #status experimental  
 F;57/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental  
 F;60/Binding site: 6-bromotryptophyl (Trp) #status experimental  
 F;63/Modified site: carbohydrate (Thr) (covalent) #status experimental  
 F;64/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 50.5%; Score 167.; DB 2; Length 67;  
 Best Local Similarity 62.3%; Pred. No. 4e-13;  
 Matches 33; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MRCLPVFVILLIITASGPVDARLTKTDDVPLSSFRDNAKSTLQRHDKSVCC 53  
 Db 1 MRCLPVFVILLIITASGPVDARLTKTDDVPLSSFRDNAKSTLQRHDKSVCC 53

RESULT 5  
 C59147 conotoxin Gm5.1 precursor - cone shell (Conus gloriamaris)  
 C;Species: Conus gloriamaris (glory-of-the-sea cone)  
 C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 19-May-2000  
 C;Accession: C59147  
 R;Walker, C.S.; Steel, D.; Jacobsen, R.B.; Lirazan, M.B.; Cruz, L.J.; Hooper, D.; Shetty J.; Biol. Chem., 274, 30664-30671, 1999  
 A;Title: The T<sub>-</sub>superfamily of conotoxins  
 A;Reference number: A59147; MUID:99452958; PMID:10521453  
 A;Accession: C59147  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-63 <WAL>  
 A;Cross-references: GB:AF167165; NID:g6103608; PIDN:AAF03685.1; PID:g6103609  
 A;Note: submitted to GenBank, July 1999  
 C;Superfamily: unassigned conotoxins  
 C;Keywords: toxin; venom  
 F;1-19/Domain: signal sequence #status predicted <SIG>  
 F;20-50/Domain: propeptide #status predicted <PRO>  
 F;51-63/Domain: conotoxin gm5 #status predicted <MAT>  
 F;52-59,53-60/Disulfide bonds: #status predicted

Query Match 44.7%; Score 148.; DB 2; Length 63;  
 Best Local Similarity 58.5%; Pred. No. 7.5e-11;  
 Matches 31; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

Qy 1 MRCLPVFVILLIITASGPVDARLTKTDDVPLSSFRDNAKSTLQRHDKSVCC 53  
 Db 1 MRCLPVFVILLIITASGPVDARLTKTDDVPLSSFRDNAKSTLQRHDKSVCC 53

RESULT 6  
 C59147 conotoxin Im5.1 precursor - cone shell (Conus imperialis)  
 C;Species: Conus imperialis (imperial cone)  
 C;Accession: C59147  
 R;Walker, C.S.; Steel, D.; Jacobsen, R.B.; Lirazan, M.B.; Cruz, L.J.; Hooper, D.; Shetty J.; Biol. Chem., 274, 30664-30671, 1999  
 A;Title: The T<sub>-</sub>superfamily of conotoxins  
 A;Reference number: A59147; MUID:99452958; PMID:10521453  
 A;Accession: C59147  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-62 <WAL>

A;Cross-references: GB:AF167169; NID:g6103616; PIDN:AAF03689.1; PID:g6103617  
 A;Note: submitted to GenBank, July 1999  
 C;Superfamily: unassigned conotoxins  
 C;Keywords: amidated carboxyl end; toxin; venom

F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:4-15/Domain: propeptide #status predicted <PRO>  
 F:4-6-10/Domain: conotoxin\_im5 #status predicted <MAT>  
 F:50-57,51-58/Disulfide bonds: #status predicted  
 F:60/Modified site: amidated carboxyl end (Trp) (amide in mature form from following gyl)

Query Match 39.1%; Score 129.5%; DB 2; Length 62;  
 Best Local Similarity 50.8%; Pred. No. 1.3e-08;  
 Matches 32; Conservative 5; Mismatches 23; Indels 3; Gaps 2;

RESULT 9  
 HNVZT  
 Query 1 MRCLPVPVILLLTAGSPVSDARLTKMDDPLSSFRDNKSTLQRHQDKSVCCGYKL-CF 59  
 Db 1 MYCLPVPVILLLISSAPSTPPQPRNKKDRVHLISLDNHKQILQR-DWNSCCGKRNPGCC 58

Qy 60 PCG 62  
 Db 59 Pwg 61

A;Title: Vaccinia virus hemagglutinin. A novel member of the immunoglobulin superfamily.  
 A;Reference number: JL0108; MUID:89328331; PMID:2754392  
 A;Accession: JL0108  
 A;Molecule type: mRNA  
 A;Residues: 1-15 <JIN>  
 C;Cross-references: GB:X15709; GB:MS7773; NID:g61313; PID:g61314  
 C;Superfamily: vaccinia virus hemagglutinin; immunoglobulin homology  
 C;Keywords: Glycoprotein; hemagglutinin; late protein; transmembrane protein  
 C;Accession: B08784  
 C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 22-Oct-2001  
 R;Karoda, M.; Oht, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogashawara, N.; Hayashi, H.; Hiramatsu, K.; Lancet 357, 1225-1240, 2001  
 A;Title: Whole genome sequencing of meticillin-resistant *Staphylococcus aureus*.  
 A;Reference number: A89758; MUID:21311952; PMID:11418146  
 A;Accession: B089784  
 A;Molecule type: DNA  
 A;Residues: 1-423 <KUR>  
 A;Cross-references: GB:BA000018; PID:gi13700130; PIDN:BAB41429.1; GSPDB:GN00149  
 A;Experimental source: strain N315  
 C;Genetics:  
 A;Gene: SA0207  
 C;Superfamily: maltose-binding protein

Query Match 19.0%; Score 63; DB 2; Length 423;  
 Best Local Similarity 31.7%; Pred. No. 8.6%;  
 Matches 13; Conservative 15; Mismatches 7; Indels 6; Gaps 2;

RESULT 10  
 H90413  
 Query 1 MRCLPVPVILLLTAGSPVSDARLTKMDDPLSSFRDNK 40  
 Db 5 LKCITLAVMILLIVTAGPN---RSKEDIDKALNKDNSK 40

A;Reference number: S74222; MUID:27061201; PMID:8905231  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-715 <KAN>  
 A;Cross-references: EMBL:D90905; GB:AB001339; NID:gi1652360; PIDN:BAA17286.1; PID:di010801  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library. June 1996

Query Match 18.7%; Score 62; DB 2; Length 715;  
 Best Local Similarity 28.0%; Pred. No. 18;  
 Matches 14; Conservative 7; Mismatches 21; Indels 8; Gaps 1;

RESULT 11  
 T13347  
 Query 20 VDARLTKMDDPLSSFRDNKSTLQRHQDKSVCCGYKL-CF 61  
 Db 577 IDVKKSTDYFLKISSQQGHILYSIINYFQLLYHNEHKSTCTGYEARFCIC 626

C;Species: Synechocystis sp. (strain PCC 6803)  
 C;Variety: PCC 6803  
 C;Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 08-Oct-1999  
 C;Accession: S77439  
 C;Accession: S77439  
 R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asami, E.; Nakamura, Y.; Miyajima, N.; O., K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanaabe, A.; Yamada, M.; Yasuda, DNA Res. 3, 109-13, 1996  
 A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*  
 A;Reference number: S74222; MUID:27061201; PMID:8905231  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-715 <KAN>  
 A;Cross-references: EMBL:D90905; GB:AB001339; NID:gi1652360; PIDN:BAA17286.1; PID:di010801  
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library. June 1996

Query Match 18.1%; Score 60; DB 2; Length 389;  
 Best Local Similarity 46.9%; Pred. No. 18;  
 Matches 15; Conservative 3; Mismatches 14; Indels 0; Gaps 0;

RESULT 12  
 T13347  
 Query 18 PSVDARLTKMDDPLSSFRDNKSTLQRHQDK 49  
 Db 138 PTVSDDTSIKDSDVPFSSFPHVTSYLVKEYQDK 169

C;Species: Magnaporthe grisea  
 C;Accession: T18347

C;Cross-references: EMBL:D90905; GB:AB001339; NID:gi1652360; PIDN:BAA17286.1; PID:di010801  
 C;Status: truncated - rice blast fungus magnaporthe gypsy retrotransposon  
 C;Accession: T18347

C;Cross-references: EMBL:D90905; GB:AB001339; NID:gi1652360; PIDN:BAA17286.1; PID:di010801  
 C;Status: truncated - rice blast fungus magnaporthe gypsy retrotransposon  
 C;Accession: T18347

C;Cross-references: EMBL:D90905; GB:AB001339; NID:gi1652360; PIDN:BAA17286.1; PID:di010801  
 C;Status: truncated - rice blast fungus magnaporthe gypsy retrotransposon  
 C;Accession: T18347

C;Cross-references: EMBL:D90905; GB:AB001339; NID:gi1652360; PIDN:BAA17286.1; PID:di010801  
 C;Status: truncated - rice blast fungus magnaporthe gypsy retrotransposon  
 C;Accession: T18347

R;Farman, M.L.; Tosa, Y.; Nitta, N.; Leong, S.A.  
Mol. Gen. Genet. 251, 665-674, 1996  
A;Title: MAGGY, a retrotransposon in the genome of the rice blast fungus Magnaporthe grisea  
A;Reference number: Z188822; PMID:96335141; PMID:87573397  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: DNA  
A;Residues: 1-457 <PAR>  
A;Cross-references: EMBL:L35053; NID:9522300; PID:9522301; PIDN:AAA33419.1  
C;Genetics:  
A;Gene: gag  
A;Mobile element: magnaporthe gypsy retrotransposon

Query Match 18.0%; Score 59.5%; DB 1; Length 2148;  
Best Local Similarity 26.8%; Pred. No. 1e+02; Indels 7; Gaps 2;  
Matches 15; Conservative 12; Mismatches 22; Indels 7; Gaps 2;

Qy 1 15 ASGPSUDARLKTKDVLSSERFDNAK-----STLQRHQDKSVCCGYKLCPG 62  
Db 339 AAAPPAPAAPTQDIPRAAPKPAALPLNDPMDLSQQREHNRKE---NMLCYRCG 391

RESULT 12

A56081 insulin receptor - fruit fly (*Drosophila melanogaster*)  
N; Contains: protein-tyrosine kinase (EC 2.7.1.-)  
C;Species: *Drosophila melanogaster*  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999  
C;Accession: A56081; A26378; A24147  
R.; Ruan, Y.; Chen, C.; Cao, Y.; Garofalo, R.S.  
J. Biol. Chem. 270, 4236-4243, 1995  
A;Title: The *Drosophila* insulin receptor contains a novel carboxyl-terminal extension li  
A;Reference number: A56081; MUID:95181404; PMID:7876183  
A;Accession: A56081  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: mRNA  
A;Residues: 1-2148 <RUA>  
A;Cross-references: GB:U18351  
R.Nishida, Y.; Hata, M.; Nishizuka, Y.; Rutter, W.J.; Ebina, Y.  
Biochem. Biophys. Res. Commun. 141, 474-481, 1986  
A;Title: Cloning of a *Drosophila* cDNA encoding a polypeptide similar to the human insuli  
A;Reference number: A26378; MUID:87100165; PMID:3099787  
A;Accession: A26378  
A;Molecule type: mRNA  
A;Residues: 656 '/PPPPP'PPL'-----'LAATI', '731-733-867-'TOL', '871-'AVT  
AQR', '1281', 'PLQLQ', '1287-1-160', 'VB', '1,163-142', 'RSGMRDDVS', '1481', 'IAWM', '1489-1-1502', 'V', '1504  
A;Cross-references: GB:U1778; NID:AA57759; PIDN:AA28644.1; PID:91760121; PMID:91760121; PMID:11679669  
R;Petruzzelli, L.; Herrera, R.; Arenas-Garcia, R.; Fernandez, R.; Birnbaum, M.J.; Rosen,  
Proc. Natl. Acad. Sci. U.S.A. 83, 4710-4714, 1986  
A;Title: Isolation of a *Drosophila* genomic sequence homologous to the kinase domain of b  
A;Reference number: A24147; MUID:86259667; PMID:3014506  
A;Accession: A24147  
A;Molecule type: DNA  
A;Residues: 'LIQQ', '1308-1476', 'DGHDVDS', '1484-1522', 'PF', '1525-1572', 'QAWCLLVPVT', '1583-1594,  
A;Cross-references: FlyBase:FBgn0013984  
C;Superfamily: Drosophila insulin receptor; protein kinase homology  
A;Experimental source: unspecified Drosophila species  
C;Genetics:  
A;Gene: Flybase:INR  
A;Cross-references: FlyBase:FBgn0013984  
C;Species: Mus musculus (house mouse)  
C;Accession: A32495; A30939  
R;Linton, J.P.; Yen, J.Y.J.; Selby, E.; Chen, Z.; Chinsky, J.M.; Liu, K.; Kellens, R.E.;

Query Match 18.0%; Score 59.5%; DB 1; Length 2148;  
Best Local Similarity 26.8%; Pred. No. 1e+02; Indels 7; Gaps 2;  
Matches 15; Conservative 12; Mismatches 22; Indels 7; Gaps 2;

Qy 1 10 LLITATAGPSVDARL-KTKDDVPLSSFRDNA-----KSTLQRHQDKSVCCGYKL 58  
Db 476 LVVLTENSKKECEKRLSKCPEIRIEEGHDNTATEGELNASCOLHNNSKLC 531

RESULT 13

T03701 SAR8.2e protein, TMV-inducible - common tobacco  
C;Species: *Nicotiana tabacum* (common tobacco)  
C;Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 24-Mar-1999  
C;Accession: T03701  
R;Ward, E.R.; Uknes, S.J.; Williams, S.C.; Dincher, S.S.; Wiederhold, D.L.; Alexander, D  
Plant Cell 3, 1085-1094, 1991  
A;Title: Coordinate gene activity in response to agents that induce systemic acquired re  
A;Reference number: Z15021  
A;Accession: T03701  
A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 1-111 <WAR>  
A;Cross-references: EMBL:M977362; NID:9170340; PID:9170341  
C;Genetics:  
A;Gene: SAR8.2e

Query Match 17.8%; Score 59; DB 2; Length 111;  
Best Local Similarity 20.8%; Pred. No. 7.7; Mismatches 22; Indels 16; Gaps 3;  
Matches 15; Conservative 19; Mismatches 22; Indels 16; Gaps 3;

Qy 3 CLPVFVILLLTASGPSVDARLTKDVLSSFRDNAKSTLQRHQDK-----S 50  
Db 10 CILSALLLIVISS-----QADABETSKATAPIQMENNNTTQPKPKPGNNIFGACK 66

Query Match 17.8%; Score 59; DB 2; Length 111;  
Best Local Similarity 20.8%; Pred. No. 7.7; Mismatches 22; Indels 16; Gaps 3;  
Matches 15; Conservative 19; Mismatches 22; Indels 16; Gaps 3;

Qy 5 CLPVFVILLLTASGPSVDARLTKDVLSSFRDNAKSTLQRHQDK-----S 50  
Db 10 CILSALLLIVISS-----QADABETSKATAPIQMENNNTTQPKPKPGNNIFGACK 66

RESULT 14

A11093 Oligopeptide ABC transporter-binding protein homolog lmo01152 [imported] - *Listeria monocytogenes*  
C;Species: *Listeria monocytogenes*  
C;Date: 27-Nov-2001 #sequence\_revision 27-Nov-2001 #text\_change 31-Dec-2001  
C;Accession: A11093  
R;Glaser, P.; Frangoul, I.; Buchriesser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker, D.; Dominguez-Bernal, G.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karet, U.; Science 294, 849-852, 2001  
A;Authors: Kreft, J.; Kahn, M.; Kunst, F.; Kurapkat, G.; Madiueno, E.; Maitouram, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, R.; Wehland, A;Title: Comparative genomics of *Listeria* species.  
A;Reference number: AB1077; MUID:21537279; PMID:11679669  
A;Accession: A11093  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-551 <GLA>  
A;Cross-references: GB:NC\_003210; PIDN:CAIC98367.1; PID:916409511; GSPDB:GN00177  
A;Experimental source: strain EGD-e  
C;Genetics:  
A;Gene: lmo01152  
C;Superfamily: dipeptide transport protein

Query Match 17.5%; Score 58; DB 2; Length 551;  
Best Local Similarity 36.0%; Pred. No. 44; Mismatches 3; Indels 20; Gaps 2;

Qy 2 RCLPVFVLL-LLTATAGPSVDARLTKDVLSSFRDNAKSTLQRHQDK 49  
Db 6 KTLPIFAITLVILLTAGC-----NDNEKSTTKTSKSPDK 37

RESULT 15

A32495 rep-1 protein, form A - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 12-Oct-1989 #sequence\_revision 12-Oct-1989 #text\_change 16-Feb-1997  
C;Accession: A32495; A30939  
R;Linton, J.P.; Yen, J.Y.J.; Selby, E.; Chen, Z.; Chinsky, J.M.; Liu, K.; Kellens, R.E.;

Mol. Cell. Biol. 9, 3058-3072, 1989  
A;Title: Dual bidirectional promoters at the mouse dhfr locus: cloning and characterization  
A;Reference number: A32495; MUID:89384567; PMID:2674679  
A;Accession: A32495  
A;Molecule type: mRNA  
A;Residues: 1-929 <LNN>  
A;Cross-references: GB:M24919; GB:J04244  
C;Genetics:  
A;Gene: rep-1  
C;Keywords: DNA binding

Query Match Similarity 17.5%; Score 58; DB 2; Length 929;  
Best Local Similarity 32.1%; Pred. No. 71;  
Matches 18; Conservative 5; Mismatches 17; Indels 16; Gaps 3;  
3;  
Qy 17 GPSVDAKLTKDDVPLSSFRDNAAKSTL-----OQHODKSVC--CGYKLCF 59  
Db 164 GPCPEVEQKTSCKP--FNKRKSKVYTPLIQLYLDMKQOHKDAVLCECGYKYRF 216

Search completed: August 10, 2004, 16:04:56  
Job time : 19.2703 secs

Blank Sheet

Result No.	Score	Query Match	Length	DB ID	Description
1	191	57.7	61	CXL2_CONMR	P58806 conus marmo
2	188	56.8	63	CX5A_CONPU	Q9u666 conus purpu
3	180.5	54.5	62	CX52_CONGL	Q9u658 conus glori
4	169.5	51.2	62	CX51_CONTE	Q9u700 conus texti
5	167	50.5	67	CXET_CONTE	P8175 conus texti
6	148	44.7	63	CX51_CONGL	Q9u729 conus glori
7	129.5	39.1	62	CX51_CONIN	Q9u665 conus imper
8	68	20.5	11	CXL1_CONWR	P58807 conus marmo
9	68	20.5	13	CXL4_CONMR	P58810 conus marmo
10	61	18.4	315	HEMA_VACCT	P16556 vaccinia vi
11	59	17.8	313	SPY2_CHICK	Q9pE12 gallus galli
12	58	17.5	1091	MSH3_MOUSE	P13705 mus musculus
13	58	17.5	1131	YANC_SCHPO	Q10077 schizorhabdi
14	58	17.5	1969	MYSA_CAEEL	P12844 caenorhabditis
15	57.5	17.4	802	PUR2 YEAST	P01244 bifunctional
16	57	17.2	323	Y370 MYCER	P4761 mycoplasma
17	57	17.2	662	PAS1_SCHAM	P10557 schistosercer
18	56.5	17.1	650	APP1_HUMAN	P51693 homo sapiens
19	56	16.9	369	YF00_SYN3	P73033 synechocystis
20	55.5	16.8	907	MOP_DESGI	Q46509 desulfobacter
21	55.5	16.8	953	CAR4_HUMAN	P97239 homo sapiens
22	55.5	16.8	1287	SK12 YEAST	P3520 saccharomyces
23	55.5	16.8	1297	SOS2_MOUSE	P03384 mus musculus
24	55	16.6	170	I2S2_ARATH	P15458 arabidopsis
25	55	16.6	185	VNS2_MOUSE	P62472 mus musculus
26	55	16.6	467	HYIN_AGRITU	P03868 agrobacterium
27	55	16.6	789	PARC_MYCEN	P75352 mycoplasma
28	55	16.6	3726	ABF1_MOUSE	P61329 mus musculus
29	54.5	16.5	266	RPOD_MEITA	Q8Pv16 methanosaeta
30	54	16.3	12	CXL3_CONNR	P58809 conus marmo
31	54	16.3	262	FIBOL_BONNO	P21828 bombyx mori
32	54	16.3	345	CLIP_PIG	Q95n03 sus scrofa
33	54	16.3	708	CAO2_CANTR	P06598 candida tro

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Lissing first 45 summaries

Database : SwissProt\_42; \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	191	57.7	61	CXL2_CONMR	P58806 conus marmo
2	188	56.8	63	CX5A_CONPU	Q9u666 conus purpu
3	180.5	54.5	62	CX52_CONGL	Q9u658 conus glori
4	169.5	51.2	62	CX51_CONTE	Q9u700 conus texti
5	167	50.5	67	CXET_CONTE	P8175 conus texti
6	148	44.7	63	CX51_CONGL	Q9u729 conus glori
7	129.5	39.1	62	CX51_CONIN	Q9u665 conus imper
8	68	20.5	11	CXL1_CONWR	P58807 conus marmo
9	68	20.5	13	CXL4_CONMR	P58810 conus marmo
10	61	18.4	315	HEMA_VACCT	P16556 vaccinia vi
11	59	17.8	313	SPY2_CHICK	Q9pE12 gallus galli
12	58	17.5	1091	MSH3_MOUSE	P13705 mus musculus
13	58	17.5	1131	YANC_SCHPO	Q10077 schizorhabdi
14	58	17.5	1969	MYSA_CAEEL	P12844 caenorhabditis
15	57.5	17.4	802	PUR2 YEAST	P01244 bifunctional
16	57	17.2	323	Y370 MYCER	P4761 mycoplasma
17	57	17.2	662	PAS1_SCHAM	P10557 schistosercer
18	56.5	17.1	650	APP1_HUMAN	P51693 homo sapiens
19	56	16.9	369	YF00_SYN3	P73033 synechocystis
20	55.5	16.8	907	MOP_DESGI	Q46509 desulfobacter
21	55.5	16.8	953	CAR4_HUMAN	P97239 homo sapiens
22	55.5	16.8	1287	SK12 YEAST	P3520 saccharomyces
23	55.5	16.8	1297	SOS2_MOUSE	P03384 mus musculus
24	55	16.6	170	I2S2_ARATH	P15458 arabidopsis
25	55	16.6	185	VNS2_MOUSE	P62472 mus musculus
26	55	16.6	467	HYIN_AGRITU	P03868 agrobacterium
27	55	16.6	789	PARC_MYCEN	P75352 mycoplasma
28	55	16.6	3726	ABF1_MOUSE	P61329 mus musculus
29	54.5	16.5	266	RPOD_MEITA	Q8Pv16 methanosaeta
30	54	16.3	12	CXL3_CONNR	P58809 conus marmo
31	54	16.3	262	FIBOL_BONNO	P21828 bombyx mori
32	54	16.3	345	CLIP_PIG	Q95n03 sus scrofa
33	54	16.3	708	CAO2_CANTR	P06598 candida tro

## ALIGNMENTS

RESULT 1					
ID	CXL2_CONMR	CONMR	STANDARD;	PRT;	61 AA.
AC	P58808;				
DT	28-FEB-2003	(Rel. 41, Created)			
DT	28-FEB-2003	(Rel. 41, Last sequence update)			
DT	28-FEB-2003	(Rel. 41, Last annotation update)			
DE	Lambda-conotoxin CMVIB precursor (Chi-conotoxin MRIA)	(Chi-MRIA)			
DB	(mrna).				
OS	Conus marmoratus (Marble cone).				
OC	Bukaryota; Metazoa; Mollusca; Gastroptoda; Orthogastropoda; Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda; Neogastropoda; Conoidea; Conidae; Conus.				
OC	NCBI-TaxID:42752;				
OX					
RN	[1]				
RP	SEQUENCE FROM N.A., SEQUENCE OF 49-61, SYNTHESIS, AND MASS SPECTROMETRY.				
RC	TISSUE=Venom, and Venom duct,				
RX	McIntosh J.M., Corpuz G.C., Layer R.T., Garrett J.E., Wagstaff J.D.,				
RA	Bulaj G., Vyazovkina A., Yoshikami D., Cruz L.J., Olivera B.M.,				
RT	"Isolation and characterization of a novel conus peptide with apparent antinociceptive activity."				
RC	SEQUENCE OF 49-61, AND MASS SPECTROMETRY.				
RX	Medline:20490650; PubMed:10900201;				
RA	Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M., Seow K.T., Bay B.-H.;				
RT	"Lambda-conotoxins, a new family of conotoxins with unique disulfide pattern and protein folding. Isolation and characterization from the venom of Conus marmoreus."				
RC	J. Biol. Chem. 275:32391-32397 (2000).				
RL	[2]				
RN					
RP	SEQUENCE OF 49-61, AND MASS SPECTROMETRY.				
RC	TISSUE=Venom;				
RX	Medline:1056325; PubMed:10388292;				
RA	Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M., Seow K.T., Bay B.-H.;				
RT	"Lambda-conotoxins, a new family of conotoxins with unique disulfide pattern and protein folding. Isolation and characterization from the venom of Conus marmoreus."				
RC	J. Biol. Chem. 275:39516-39522 (2000).				
RL	[3]				
RN					
RP	SEQUENCE OF 49-61, SYNTHESIS, MASS SPECTROMETRY, AND STRUCTURE BY NMR.				
RC	TISSUE=Venom;				
RX	Medline:21419681; PubMed:11528421;				
RA	Arkins A., Palant E., Craik D.J., Adams D.J., Alewood P.F., Lewis R.J.;				
RT	"Two new classes of conopeptides inhibit the alpha1-adrenoceptor and noradrenaline transporter."				
RL	Nat. Neurosci. 4:302-307 (2001).				
CC	-I- FUNCTION: Inhibits the neuronal noradrenaline transporter.				
CC	-I- SUBCELLULAR LOCATION: Secreted.				
CC	-I- TISSUE SPECIFICITY: Expressed by the venom duct.				
CC	-I- PTM: Exists in two forms, due to cis-trans isomerization at His-59-60.				
CC	-I- MASS SPECTROMETRY: MW=1408.5; METHOD=Electrospray.				
DR	Interpro: IPR00214; Conotoxin.				
PRam	PF02930; Conotoxin.				
KW	Neurotoxin; Toxin; Hydroxylation; Signal.				
FT	SIGNAL 1				
PROPEP	POTENTIAL. PROPEP 20 48				

FT PEPTIDE	49	61	LAMBDA-CONOTOXIN CMRVIB.	FT PEPTIDE	51	62	CONOTOXIN P5A.
FT DISULFID	52	61		FT DISULFID	52	59	
FT DISULFID	53	58		FT DISULFID	53	60	AMIDATION (G-63 PROVIDE AMIDE GROUP).
FT MOD_RES	60	60	HYDROXYLATION.	FT MOD_RES	62	62	
SQ SEQUENCE	61 AA;	6499 MW;	F4DE5B5A97EB8DBA CRC64;	SQ SEQUENCE	63 AA;	7102 MW;	82A8478C13D7E9 CRC64;
Query Match	57.7%	Score 191;	DB 1; Length 61;	Query Match	56.8%	Score 188;	DB 1; Length 63;
Best Local Similarity	62.3%	Pred. No. 2.8e-17;	Mismatches 4; Indels 0;	Best Local Similarity	71.7%	Pred. No. 6.8e-17;	Gaps 0;
Matches 38; Conservative				Matches 38; Conservative	2;	Mismatches 13; Indels 0;	
Qy 1 MRCLPVFVILLILTAGSPVDAIRLKTDYPLSSFRDNAAKSTLQRHQDKSVCYCGYKLCP 60				Qy 1 MRCLPVFVILLILTAGSPVDAIRLKTDYPLSSFRDNAAKSTLQRHQDKSVCYCGYKLCP 53			
Db 1 MRCLPVFVILLILTAGSPVDAIRLKTDYPLSSFRDNAAKSTLQRHQDKSVCYCGYKLCP 60				Db 1 MRCLPVFVILLILTAGSPVDAIRLKTDYPLSSFRDNAAKSTLQRHQDKSVCYCGYKLCP 53			
Qy 61 C 61				RESULT 3			
Db 61 C 61				CX52 CONGL	STANDARD;	PRT;	62 AA.
AC Q9U62B;				ID CX52 CONGL			
AC Q9U62B;				AC Q9U62B;			
DT 28-FEB-2003 (Rel. 41, Created)				DT 28-FEB-2003 (Rel. 41, Last sequence update)			
DT 28-FEB-2003 (Rel. 41, Last sequence update)				DT 15-MAR-2004 (Rel. 43, Last annotation update)			
DT 15-MAR-2004 (Rel. 43, Last annotation update)				DE Putative conotoxin GM5.2 precursor.			
DE Conotoxin P5a precursor.				OS Conus gloriamaris (Glory of the sea).			
OS Conus purpurascens (Purple cone).				OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;			
OC Conus; Neacea; Molluscs; Gastropoda; Orthogastropoda;				OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;			
OC Neogastropoda; Conoidea; Conidae; Conus.				OC Neogastropoda; Conoidea; Conidae; Conus.			
OX NCBI_TAXID=1690;				OX NCBITAXID=37336;			
RN [1]				RN SEQUENCE FROM N.A.			
RP SEQUENCE FROM N.A., SEQUENCE OF 51-62, MASS SPECTROMETRY, AND				RC TISSUE-Venom duct;			
RP SYNTHESIS.				RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,			
RX TISSUE-NAME, and Venom duct;				RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,			
RP BANDYOPADHYAY P.; CRAIG A.G.; OLIVERA B.M.;				RA Bandyopadhyay P., Craig A.G., Olivera B.M.;			
RP "The T superfamily of conotoxins.";				RA J. Biol. Chem. 274:36030-36030(1999).			
RA MEDLINE:99452958; PubMed:10521453;				RL -1 FUNCTION: Not known. Has only been studied at nucleotidic level.			
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,				CC -1 SUBCELLULAR LOCATION: Secreted.			
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;				CC -1 TISSUE SPECIFICITY: Expressed by the venom duct.			
RA "The T superfamily of conotoxins.";				CC -1 SIMILARITY: Belongs to the conotoxin T superfamily.			
RL [2]				CC -1 SIMILARITY: Belongs to the conotoxin T superfamily.			
RA ERRATUM.				CC This SWISS-PROT entry is copyright. It is produced through a collaboration			
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,				CC between the Swiss Institute of Bioinformatics and the EMBL outstation -			
RA Hooper D., Shetty R., DelaCruz R.C., Nielsen J.S., Zhou L.M.,				CC the European Bioinformatics Institute. There are no restrictions on its			
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;				CC use by non-profit institutions as long as its content is in no way			
RA "The T superfamily of conotoxins.";				CC modified and this statement is not removed. Usage by and for commercial			
RL [2]				CC entities requires a license agreement (See http://www.isb-sib.ch/announce/			
RA ERRATUM.				CC or send an email to license@isb-sib.ch).			
RA Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J.,				CC EMBL: AF167166; AA03686.1; -.			
RA Bandyopadhyay P., Craig A.G., Olivera B.M.;				DR PIR: D59147; D59147;			
RA "The T superfamily of conotoxins.";				DR InterPro; IPR004214; Conotoxin.			
RL [2]				DR Pfam; PF02950; Conotoxin; 1.			
RA ERRATUM.				KW Toxin; Signal; Amidation.			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration				CC POTENTIAL.			
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -				CC BY SIMILARITY.			
CC the European Bioinformatics Institute. There are no restrictions on its				CC use by non-profit institutions as long as its content is in no way			
CC display in this fish in response to their reflection when placed				CC modified and this statement is not removed. Usage by and for commercial			
CC in a mirrored aquarium. High levels of the peptide suppressed this				CC entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC behavior. No effect is observed when injected into mice.				CC or send an email to license@isb-sib.ch).			
CC -1 SUBCELLULAR LOCATION: Secreted.				CC DR PIR: AF167168; AA03688.1; -.			
CC -1 TISSUE SPECIFICITY: Expressed by the venom duct.				DR Pfam; PF02950; Conotoxin.			
CC -1 SIMILARITY: Belongs to the conotoxin T superfamily.				DR Toxin; Amidation; Signal.			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration				CC POTENTIAL.			
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -				CC BY SIMILARITY.			
CC the European Bioinformatics Institute. There are no restrictions on its				CC use by non-profit institutions as long as its content is in no way			
CC display in this fish in response to their reflection when placed				CC modified and this statement is not removed. Usage by and for commercial			
CC in a mirrored aquarium. High levels of the peptide suppressed this				CC entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC behavior. No effect is observed when injected into mice.				CC or send an email to license@isb-sib.ch).			
CC -1 SUBCELLULAR LOCATION: Secreted.				CC DR PIR: AF167168; AA03688.1; -.			
CC -1 TISSUE SPECIFICITY: Expressed by the venom duct.				DR Pfam; PF02950; Conotoxin.			
CC -1 SIMILARITY: Belongs to the conotoxin T superfamily.				DR Toxin; Amidation; Signal.			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration				CC POTENTIAL.			
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -				CC BY SIMILARITY.			
CC the European Bioinformatics Institute. There are no restrictions on its				CC use by non-profit institutions as long as its content is in no way			
CC display in this fish in response to their reflection when placed				CC modified and this statement is not removed. Usage by and for commercial			
CC in a mirrored aquarium. High levels of the peptide suppressed this				CC entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC behavior. No effect is observed when injected into mice.				CC or send an email to license@isb-sib.ch).			
CC -1 SUBCELLULAR LOCATION: Secreted.				CC DR PIR: AF167168; AA03688.1; -.			
CC -1 TISSUE SPECIFICITY: Expressed by the venom duct.				DR Pfam; PF02950; Conotoxin.			
CC -1 SIMILARITY: Belongs to the conotoxin T superfamily.				DR Toxin; Amidation; Signal.			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration				CC POTENTIAL.			
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -				CC BY SIMILARITY.			
CC the European Bioinformatics Institute. There are no restrictions on its				CC use by non-profit institutions as long as its content is in no way			
CC display in this fish in response to their reflection when placed				CC modified and this statement is not removed. Usage by and for commercial			
CC in a mirrored aquarium. High levels of the peptide suppressed this				CC entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC behavior. No effect is observed when injected into mice.				CC or send an email to license@isb-sib.ch).			
CC -1 SUBCELLULAR LOCATION: Secreted.				CC DR PIR: AF167168; AA03688.1; -.			
CC -1 TISSUE SPECIFICITY: Expressed by the venom duct.				DR Pfam; PF02950; Conotoxin.			
CC -1 SIMILARITY: Belongs to the conotoxin T superfamily.				DR Toxin; Amidation; Signal.			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration				CC POTENTIAL.			
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -				CC BY SIMILARITY.			
CC the European Bioinformatics Institute. There are no restrictions on its				CC use by non-profit institutions as long as its content is in no way			
CC display in this fish in response to their reflection when placed				CC modified and this statement is not removed. Usage by and for commercial			
CC in a mirrored aquarium. High levels of the peptide suppressed this				CC entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC behavior. No effect is observed when injected into mice.				CC or send an email to license@isb-sib.ch).			
CC -1 SUBCELLULAR LOCATION: Secreted.				CC DR PIR: AF167168; AA03688.1; -.			
CC -1 TISSUE SPECIFICITY: Expressed by the venom duct.				DR Pfam; PF02950; Conotoxin.			
CC -1 SIMILARITY: Belongs to the conotoxin T superfamily.				DR Toxin; Amidation; Signal.			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration				CC POTENTIAL.			
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -				CC BY SIMILARITY.			
CC the European Bioinformatics Institute. There are no restrictions on its				CC use by non-profit institutions as long as its content is in no way			
CC display in this fish in response to their reflection when placed				CC modified and this statement is not removed. Usage by and for commercial			
CC in a mirrored aquarium. High levels of the peptide suppressed this				CC entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC behavior. No effect is observed when injected into mice.				CC or send an email to license@isb-sib.ch).			
CC -1 SUBCELLULAR LOCATION: Secreted.				CC DR PIR: AF167168; AA03688.1; -.			
CC -1 TISSUE SPECIFICITY: Expressed by the venom duct.				DR Pfam; PF02950; Conotoxin.			
CC -1 SIMILARITY: Belongs to the conotoxin T superfamily.				DR Toxin; Amidation; Signal.			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration				CC POTENTIAL.			
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -				CC BY SIMILARITY.			
CC the European Bioinformatics Institute. There are no restrictions on its				CC use by non-profit institutions as long as its content is in no way			
CC display in this fish in response to their reflection when placed				CC modified and this statement is not removed. Usage by and for commercial			
CC in a mirrored aquarium. High levels of the peptide suppressed this				CC entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC behavior. No effect is observed when injected into mice.				CC or send an email to license@isb-sib.ch).			
CC -1 SUBCELLULAR LOCATION: Secreted.				CC DR PIR: AF167168; AA03688.1; -.			
CC -1 TISSUE SPECIFICITY: Expressed by the venom duct.				DR Pfam; PF02950; Conotoxin.			
CC -1 SIMILARITY: Belongs to the conotoxin T superfamily.				DR Toxin; Amidation; Signal.			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration				CC POTENTIAL.			
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -				CC BY SIMILARITY.			
CC the European Bioinformatics Institute. There are no restrictions on its				CC use by non-profit institutions as long as its content is in no way			
CC display in this fish in response to their reflection when placed				CC modified and this statement is not removed. Usage by and for commercial			
CC in a mirrored aquarium. High levels of the peptide suppressed this				CC entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC behavior. No effect is observed when injected into mice.				CC or send an email to license@isb-sib.ch).			
CC -1 SUBCELLULAR LOCATION: Secreted.				CC DR PIR: AF167168; AA03688.1; -.			
CC -1 TISSUE SPECIFICITY: Expressed by the venom duct.				DR Pfam; PF02950; Conotoxin.			
CC -1 SIMILARITY: Belongs to the conotoxin T superfamily.				DR Toxin; Amidation; Signal.			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration				CC POTENTIAL.			
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -				CC BY SIMILARITY.			
CC the European Bioinformatics Institute. There are no restrictions on its				CC use by non-profit institutions as long as its content is in no way			
CC display in this fish in response to their reflection when placed				CC modified and this statement is not removed. Usage by and for commercial			
CC in a mirrored aquarium. High levels of the peptide suppressed this				CC entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC behavior. No effect is observed when injected into mice.				CC or send an email to license@isb-sib.ch).			
CC -1 SUBCELLULAR LOCATION: Secreted.				CC DR PIR: AF167168; AA03688.1; -.			
CC -1 TISSUE SPECIFICITY: Expressed by the venom duct.				DR Pfam; PF02950; Conotoxin.			
CC -1 SIMILARITY: Belongs to the conotoxin T superfamily.				DR Toxin; Amidation; Signal.			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration				CC POTENTIAL.			
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -				CC BY SIMILARITY.			
CC the European Bioinformatics Institute. There are no restrictions on its				CC use by non-profit institutions as long as its content is in no way			
CC display in this fish in response to their reflection when placed				CC modified and this statement is not removed. Usage by and for commercial			
CC in a mirrored aquarium. High levels of the peptide suppressed this				CC entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC behavior. No effect is observed when injected into mice.				CC or send an email to license@isb-sib.ch).			
CC -1 SUBCELLULAR LOCATION: Secreted.				CC DR PIR: AF167168; AA03688.1; -.			
CC -1 TISSUE SPECIFICITY: Expressed by the venom duct.				DR Pfam; PF02950; Conotoxin.			
CC -1 SIMILARITY: Belongs to the conotoxin T superfamily.				DR Toxin; Amidation; Signal.			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration				CC POTENTIAL.			
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -				CC BY SIMILARITY.			
CC the European Bioinformatics Institute. There are no restrictions on its				CC use by non-profit institutions as long as its content is in no way			
CC display in this fish in response to their reflection when placed				CC modified and this statement is not removed. Usage by and for commercial			
CC in a mirrored aquarium. High levels of the peptide suppressed this				CC entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC behavior. No effect is observed when injected into mice.				CC or send an email to license@isb-sib.ch).			
CC -1 SUBCELLULAR LOCATION: Secreted.				CC DR PIR: AF167168; AA03688.1; -.			
CC -1 TISSUE SPECIFICITY: Expressed by the venom duct.				DR Pfam; PF02950; Conotoxin.			
CC -1 SIMILARITY: Belongs to the conotoxin T superfamily.				DR Toxin; Amidation; Signal.			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration				CC POTENTIAL.			
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -				CC BY SIMILARITY.			
CC the European Bioinformatics Institute. There are no restrictions on its				CC use by non-profit institutions as long as its content is in no way			
CC display in this fish in response to their reflection when placed				CC modified and this statement is not removed. Usage by and for commercial			
CC in a mirrored aquarium. High levels of the peptide suppressed this				CC entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC behavior. No effect is observed when injected into mice.				CC or send an email to license@isb-sib.ch).			
CC -1 SUBCELLULAR LOCATION: Secreted.				CC DR PIR: AF167168; AA03688.1; -.			
CC -1 TISSUE SPECIFICITY: Expressed by the venom duct.				DR Pfam; PF02950; Conotoxin.			
CC -1 SIMILARITY: Belongs to the conotoxin T superfamily.				DR Toxin; Amidation; Signal.			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration				CC POTENTIAL.			
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -				CC BY SIMILARITY.			
CC the European Bioinformatics Institute. There are no restrictions on its				CC use by non-profit institutions as long as its content is in no way			
CC display in this fish in response to their reflection when placed				CC modified and this statement is not removed. Usage by and for commercial			
CC in a mirrored aquarium. High levels of the peptide suppressed this				CC entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC behavior. No effect is observed when injected into mice.				CC or send an email to license@isb-sib.ch).			
CC -1 SUBCELLULAR LOCATION: Secreted.				CC DR PIR: AF167168; AA03688.1; -.			
CC -1 TISSUE SPECIFICITY: Expressed by the venom duct.				DR Pfam; PF02950; Conotoxin.			
CC -1 SIMILARITY: Belongs to the conotoxin T superfamily.				DR Toxin; Amidation; Signal.			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration				CC POTENTIAL.			
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -				CC BY SIMILARITY.			
CC the European Bioinformatics Institute. There are no restrictions on its				CC use by non-profit institutions as long as its content is in no way			
CC display in this fish in response to their reflection when placed</td							

RESULT 4		CX51_CONTE		STANDARD;		PRT;	62 AA.
Quy	1	MRCLPVFTVILLITASGPSSYDARLTKDDVPLSSFRDNAKSTLQRHQDKSVC	53				
Db	1	MRCLPVFTVILLITASAPSVDQPKTKDDVPLAFLHDNIRSTLQLR-KKYCC	52				
<b>SEQUENCE FROM N.A.</b>							
TISSUE=Venom duct; MEDLINE=99452955; PubMed=10521453;							
ID	CX51_CONTE	AC	Q9U700;	DT	28-FEB-2003 (Rel. 41, Created)		
		DT		DT	28-FEB-2003 (Rel. 41, Last sequence update)		
		DT		DT	15-MAR-2004 (Rel. 43, Last annotation update)		
		DB		DB	Putative conotoxin Tx-1 precursor.		
		OC		OC	Conus textile (Cloth-of-gold cone).		
		OC		OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;		
		OC		OC	Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;		
		NCBI		NCBI	Neogastropoda; Conoidea; Conidae; Conus.		
		OX		OX	NCBI_TaxID=6494;		
		RN		RN	[1]		
		RP		RP	SEQUENCE FROM N.A.		
		RP		RP	ERRATUM.		
		RP		RP	Walker C.S., Steel D., Jacobsen R.B., Lirazan M.B., Cruz L.J., Hooper D., Shetty R., Delaruz R.C., Nielsen J.S., Zhou L.M., Hooper D., Shetty R., Craig A.G., Oliveira B.M.;		
		RA		RA	Bandyopadhyay P., Craig A.G., Oliveira B.M.;		
		RA		RA	J. Biol. Chem. 274:36030-36030(1999).		
		RA		RA	- - FUNCTION: Not known. It has only been studied at nucleotidic level.		
		CC		CC	- - SUBCELLULAR LOCATION: Secreted.		
		CC		CC	- - TISSUE SPECIFICITY: Expressed by the venom duct.		
		CC		CC	- - SIMILARITY: Belongs to the conotoxin T-superfamily.		
		CC		CC	-----		
		CC		CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation of the European Bioinformatics Institute. There are no restrictions use by non-profit institutions. This statement is not removed, as long as its content is in modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch">http://www.isb-sib.ch</a> ) or send an email to license@isb-sib.ch).		
		CC		CC	-----		
		CC		CC	EMBL; AF067164; AA03684; 1; -.		
		CC		CC	PTB; B53147; B59147.		
		CC		CC	InterPro; IPR04214; Conotoxin.		
		CC		CC	PFam; PF02950; Conotoxin_1.		
		CC		CC	Toxin; Signal; Amidation.		
		CC		CC	SIGNAL 1 22 POTENTIAL.		
		CC		CC	PROPEP 23 48 BY SIMILARITY.		
		CC		CC	PRETIDE 49 60 PUTATIVE CONOTOXIN TX-1.		
		CC		CC	DISULFID 50 57 BY SIMILARITY.		
		CC		CC	DISULFID 51 58 BY SIMILARITY.		
		CC		CC	MOD_RES 60 60 AMIDATION (G-61 PROVIDE AMIDE GROUP)		
		CC		CC	-----		
		CC		CC	SEQUENCE 62 AA; 6857 MW; CE29803DEBODA421 CRC64;		
		CC		CC	-----		
		CC		CC	Query Match 51.2%; Score 169.5; DB 1; Length 62;		
		CC		CC	Best Local Similarity 63.8%; Pred. No. 1..4e-14; Indels 1; Gap		
		CC		CC	Matches 37; Conservative 5; Mismatches 15;		
		CC		CC	Indels 1; Gap		
		CC		CC	-----		
		CC		CC	1 MRCLPVFTVILLITASGPSSYDARLTKDDVPLSSFRDNAKSTLQRHQDKSVC		
		CC		CC	1 MCCLPVFTVILLITASAPSVDQPKTKDDVPLAFLHDNIRSTLQLR-KKYCC		



FT MOD\_RES 60 60 AMIDATION (G-61 PROVIDE AMIDE GROUP)  
 SQ SEQUENCE 62 AA; 7030 MW; 9570E7C02275796D CRC64;

Query Match 39.1%; Score 129.5; DB 1; Length 62;  
 Best Local Similarity 50.8%; Pred. No. 1; 5e-09;  
 Matches 32; Conservative 5; Mismatches 23; Indels 3; Gaps 2;

Qy 1 MRCLPVFVILLITASGPVDARLTKTQDVPLSSFRDNKSTLQRHQDKNSVCGYKL-CF 59  
 Db 1 MYCLPVFVILLITASSPSTPPQFRNKDRVHLISLLNPKTILQR-DWNSCCGKNPGCC 58

Qy 60 PCG 62  
 Db 59 PWG 61

---

RESULT 8  
 CXL1 CONMR ID \_CXL1 CONMR STANDARD; PRT; 11 AA.  
 AC P58807; DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Lambda-conotoxin CMrVTA.  
 OS Conus marmoreus (Marble cone).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;  
 OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 NCBI\_TaxID=42755;  
 RN SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.  
 RC TISSUE=Venom;  
 RX MEDLINE=20564325; PubMed=10988292;  
 RA Balaji R.A., Ohnake A., Sato K., Gopalakrishnakone P., Kini R.M.,  
 RA Seow K.T., Bay B.-H.;  
 RT "Lambda-conotoxins, a new family of conotoxins with unique disulfide  
 pattern and protein folding. Isolation and characterization from the  
 venom of *Conus marmoreus*.";  
 RT J. Biol. Chem. 275:39516-39522(2000).  
 RL 275:39516-39522(2000).  
 CC -|- FUNCTION: Inhibits the neuronal noradrenaline transporter.  
 CC -|- SUBCELLULAR LOCATION: Secreted.  
 CC -|- TISSUE SPECIFICITY: Expressed by the venom duct.  
 CC -|- MASS SPECTROMETRY: MW=1237.93; MW\_ERR=0.21; METHOD=Electrospray.  
 CC -|- SIMILARITY: Belongs to the chi/lambda-conotoxin family.  
 KW Neurotoxin; Toxin; Hydroxylation.  
 FT DISULFID 2 11  
 FT DISULFID 3 8 HYDROXYLATION.  
 FT MOD\_RES 10 10 HYDROXYLATION.  
 SQ SEQUENCE 11 AA; 1226 MW; 277AAC60B732B58 CRC64;

Query Match 20.5%; Score 68; DB 1; Length 11;  
 Best Local Similarity 90.9%; Pred. No. 0.013;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 51 VCCGYKLCFPC 61  
 Db 1 VCCGYKLCHPC 11

---

RESULT 10  
 HEMA\_VACCT ID HEMA\_VACCT STANDARD; PRT; 315 AA.  
 AC P16561; DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Hemagglutinin precursor.  
 GN HA.Or.A56R.  
 OS vaccinia virus (strain Tian Tan).  
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
 OC Orthopoxvirus.  
 OC  
 RN [1] — TAXID=10233;  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=8332831; PubMed=2754392;  
 RA Dongyan J., Zhiiliang L., Qi J., Hao Y., Yunde H.;  
 RT "Vaccinia virus hemagglutinin. A novel member of the immunoglobulin  
 superfamily.";  
 RT J. Exp. Med. 170:571-576(1989).  
 RL -|- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -|- PTM: Glycosylation: contains phosphate and sulfate-substituted  
 glycans. O-glycosylation is required for hemagglutination and  
 hemadsorption activities of infected cell membranes.  
 CC -|- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

---

CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 CC or send an email to license@isb-sib.ch).

---

CC DR EMBL; X15709; CAA37401; -  
 CC DR PIR; JU0109; IINVZT;  
 CC DR InterPro; IPR007110; Ig-like.  
 CC DR InterPro; IPR003599; Ig.  
 CC DR Pfam; PF00047; ig\_1.  
 CC DR SMART; SM00409; Ig\_1.

DR PROSITE; PS50815; IG\_LIKE; 1.  
 KW Hemagglutinin; Envelope protein; Glycoprotein; Signal;  
 KW Transmembrane; Immunoglobulin domain.  
 FT SIGNAL; 1 16 HEMAGGLUTININ.  
 FT CHAIN; 17 315 EXTRACELLULAR (POTENTIAL).  
 FT TRANMEM 17 279 POTENTIAL.  
 FT DOMAIN 280 303 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 304 315 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 17 121 IG-LIKE V-TYPE.  
 FT DISULFID 34 103 POTENTIAL.  
 FT CARBOHYD 37 37 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 254 254 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 315 AA; 34772 MW; E049448640879FF4 CRC64;

Query Match 18.4%; Score 61; DB 1; Length 315;  
 Best Local Similarity 39.5%; Pred. No. 3.7; Matches 5; Mismatches 18; Indels 0; Gaps 0;

Matches 15; Conservative 16; Score 59; DB 1; Length 313;  
 Matches 16; Conservative 9; Mismatches 26; Indels 2; Gaps 1;

Qy 1 MRCLPVVILLIATGGPSVDAKLTKTDDVPLSSFRDN 38  
 1 MARLPILLISLIVYSTRSPQTSKKIGDATLSCNERN 38

Db 11 ILLITASGPSPVDA-ARLKTKDDVPLSSFRDNAKSTLQRHQDKSVCCGYKLCPFC 61  
 135 LIGSSSSGPVADGIVRMOPKSEIKSEKPLSKEDGAHSYRCEDCGKCKC 61

RESULT 11  
 SPY2\_CHICK STANDARD; ERT; 313 AA.

AC Q9PTL2  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Sprouty homolog 2 (Spry-2).  
 GN SPRY2.  
 OC Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Archosauvia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
 OC  
 NCBI\_TAXID=9031;  
 RN RP SEQUENCE FROM N.A.  
 RX MEDLINE=99429807; PubMed=10498682;  
 RA Minowada G., Jaris L.A., Chi C.L., Neubuser A., Sun X., Hacohen N.,  
 RA Krasnow M.A., Martin G.R.;  
 RT "vertebrate sprouty genes are induced by FGF signaling and can cause  
 chondrodysplasia when overexpressed.",  
 RT Development 126:4465-4475(1999).  
 [2]  
 RN RP SEQUENCE FROM N.A.  
 RX MEDLINE=2013796; PubMed=10662503;  
 RA Chambers D., Medhurst A.D., Walsh F.S., Price J., Mason I.;  
 RA "Differential display of genes expressed at the midbrain/hindbrain  
 junction identifies sprouty2: an FGF8-inducible member of a family of  
 intracellular FGF antagonists.",  
 RT Mol. Cell. Neurosci. 15:22-35(2000).  
 CC -!- FUNCTION: May play an important role in FGF-mediated patterning of  
 CC the mid/hindbrain region by acting to modulate the signaling  
 CC effects of FGF8 through participation in a regulatory negative  
 CC feedback loop.  
 CC -!- SUBCELLULAR LOCATION: FOUND IN THE CYTOPLASM IN UNSTIMULATED CELLS  
 CC WITH FGF (EPIDERMAL GROWTH FACTOR).  
 CC -!- TISSUE SPECIFICITY: Brain and interlimb region.  
 CC -!- DEVELOPMENTAL STAGE: At the 4- to 5-somite stage (4/5S) found in  
 CC the embryo in scattered cells across the neural plate in the  
 CC presumptive mid/ hindbrain region. At 7/8S found in the isthmus  
 CC and throughout the presumptive rh territory. Between 10-14S stage  
 CC found throughout the R1 region and at the isthmic constriction. By  
 CC 26S the anterior limit of expression extends into the posterior  
 CC midbrain region and this pattern of expression is maintained at  
 CC later stages.

RESULT 12  
 MSH3\_MOUSE STANDARD; PRT; 1091 AA.

AC P13705  
 ID MSH3\_MOUSE  
 AC P13705;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE DNA mismatch repair protein Msh3 (Repair-3 protein) (REP-1).  
 DE MSH3 OR REP-3.  
 GS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 OC  
 NCBI\_TAXID=10090;  
 RN RP SEQUENCE FROM N.A.  
 RA Liu K., Niu L., Linton J.P., Crouse G.F.;  
 RA Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.  
 RN RP SEQUENCE FROM N.A.  
 RA Liu K., Niu L., Linton J.P., Crouse G.F.;  
 RA Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.  
 RN RP SEQUENCE FROM N.A.  
 RX MEDLINE=95011610; PubMed=7926796;  
 RN RP SEQUENCE OF 1-917 FROM N.A.  
 RA Liu K., Niu L., Linton J.P., Crouse G.F.;  
 RA "Characterization of the mouse Rep-3 gene: sequence similarities to  
 RT bacterial and yeast mismatch-repair proteins.";  
 RA Linton J.P., Yen J.-Y.J., Selby E., Chen Z., Chinsky J.M., Liu K.,  
 RA Kellens R.E.; Crouse G.F.;  
 RT "Dual bidirectional promoters at the mouse dhfr locus: cloning and  
 RT characterization of two mRNA classes of the divergently transcribed  
 RT Rep-1 gene.";  
 RT Mol. Cell. Biol. 9:3059-3072(1989).  
 CC -!- FUNCTION: NOT KNOWN. PROBABLE DNA REPAIR PROTEIN  
 CC -!- SIMILARITY: Belongs to the DNA mismatch repair mutS family.

RESULT 13  
 This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
 use by non-profit institutions as long as its content is in no way  
 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See http://www.isb-sib.ch/announce/  
 or send an email to license@isb-sib.ch).



SEQUENCE FROM N.A.	
RP STRAIN=Bristol N2;	RHarris B.R./ Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
RX MEDLINE=89178677; PubMed=2926820;	
RA Dibb N.J., Maruyama I.N., Krause M., Karn J.;	"Sequence analysis of the complete Caenorhabditis elegans myosin heavy chain gene family." RT
RT J. Mol. Biol. 205:603-613 (1989). RT	[2]
RN RP SEQUENCE FROM N.A.	
RC STRAIN=Bristol N2;	RHarris B.R./ Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases
RA CC -1- FUNCTION: Muscle contraction.	
CC -1- SUBUNIT: Muscle myosin is a hexameric protein that consists of 6 heavy chain subunits (MHC), 2 alkali light chain subunits (MLC1) and 2 regulatory light chain subunits (MLC2).	
CC -1- SUBCELLULAR LOCATION: Thick filaments of the myofibrils.	
CC -1- DOMAIN: The rodlike tail sequence is highly repetitive, showing cycles of a 28-residue repeat pattern composed of 4 heptapeptide repeats characteristic for alpha-helical coiled coils.	
CC -1- MISCELLANEOUS: Each myosin heavy chain can be split into 1 light meromyosin (LM) and 1 heavy meromyosin (HM). It can later be split further into 2 globular subfragments (S1) and 1 rod-shaped subfragment (S2).	
CC -1- MISCELLANEOUS: There are four different myosin heavy chains in C.elegans.	
CC -1- MISCELLANEOUS: MHC A and MHC B are found exclusively in the body wall muscle. They co-assemble into body wall thick filament.	
CC -1- SIMILARITY: Contains 1 myosin-like globular head domain.	
CC -1- SIMILARITY: Contains 1 IQ domain.	
CC CC This SWISS-PROT entry is copyright. It is produced through a collab-	
CC between the Swiss Institute of Bioinformatics and the EMBL out-	
CC wall muscle. They co-assemble into body wall thick filament.	
CC use by non-profit institutions as long as its content is in	
CC modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/">http://www.isb-sib.ch/</a> or send an email to license@isb-sib.ch).	
CC EMBL; X08067; CBA30856.1; -.	
DR EMBL; Z78199; CB01576.1; -.	
DR PIR; T23622; S02771.	
DR HSSP; P08199; 1MND.	
DR WormPep; KL12F2.1.; CE12204.	
DR InterPro; IPR000048; IQ_region.	
DR InterPro; IPR000609; myosin_head.	
DR InterPro; IPR004009; Myosin_N.	
DR InterPro; IPR002928; Myosin_tail.	
DR Pfam; PF00612; IQ_1.	
DR Pfam; PF00063; myosin_head; 1.	
DR Pfam; PF02736; Myosin_N; 1.	
DR Pfam; PF01576; Myosin_tail; 1.	
DR PRINTS; PRO193; MYOSINHEAVY.	
DR ProDom; PD000355; myosin_head; 1.	
DR SMART; SM00015; IQ_1.	
DR SMART; SM0242; Msc; 1.	
DR PROSITE; PS50096; IQ_1.	
KW Myosin; Muscle protein; Coiled coil; Thick filament; Actin-bindin-	
KW ATP-binding; Methylation; Multigene family.	
FT DOMAIN 1 793 MYOSIN HEAD-LIKE.	
FT DOMAIN 1 794 823 COILED COIL (POTENTIAL).	
FT DOMAIN 857 1969 COILED COIL (POTENTIAL).	
FT NP_BIND 179 186 ACTIN-BINDING.	
FT DOMAIN 667 689 ACTIN-BINDING.	
FT DOMAIN 770 784 METHYLATION (TRI-) (POTENTIAL).	
FT MOD_RES 130 130 Y -> YVRKLRFLFKCKINTIQQLRNRFQ (IN R	
FT CONFLICT 116 116 2).	
FT SEQUENCE 1969 AA; 225509 MW; 64577BBAF7EAD80A CRC64;	
SQ Query Match 17.5%; Score 58; DB 1; Length 1969;	
Best Local Similarity 27.1%; Pred. No. 63;	
Matches 13; Conservative 12; Mismatches 21; Indels 2;	

Qy	2 RCLPVFVILLTASGSPSYDARLKTKDVPPLSSFRDNAKSTLQRHQDK 49	
Db	284 RCHHFF-YQIMSGNDPSSLRKULNSNDITYYHFCSQAELTBGMDDK 329	
<b>RESULT 15</b>		
PUR2 YEAST	STANDARD;	
ID	PUR2 YEAST	
AC	P072744;	
DT	01-APR-1988 (Rel. 07, Created); 01-APR-1988 (Rel. 43, Last annotation update)	
DT	15-MAR-2004 (Rel. 43, Last annotation update)	
DB	Bi-functional purine biosynthetic protein ADES_7 [Includes: Glycine ligase (EC 6.3.4.13) (GARS) (Glycine--Glycylamidine synthetase) (Phosphoribosylglycynamide synthetase); Phosphoribosylformylglycynamidine cyclo-ligase (EC 6.3.3.1) (Phosphoribosyl-aminoimidazole synthetase) (AIR synthase)].	
DE	ADES_7 OR YGL234W.	
OS	Saccharomyces cerevisiae (Baker's yeast).	
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes.	
OC	Saccharomycetales; Saccharomycetaceae; Saccharomyces.	
OX	NCBI_TaxID:4932;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	Medline=87061006; PubMed=3097325;	
RA	Henikoff S.; Hartmann B., Kramer B., Kermorgant M., Monribot C., Slonimski P.; Dujardin G., Kermer M., Monribot C., Slonimski P.; Boucherie H., Dujardin G., Kermorgant M., Monribot C., Slonimski P.; Perrot M.; Boucherie H., Dujardin G., Kermorgant M., Monribot C., Slonimski P.; RT "Two-dimensional protein map of <i>Saccharomyces cerevisiae</i> : construction of a gene-protein index.";	
RT	RT overlapping Drosophila melanogaster Gart polypeptides.;	
RT	RT	
RL	J. Mol. Biol. 190:519-528(1986).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RA	Kermorgant M., Monribot C., Slonimski P.; Hartmann B., Kramer B., Kermorgant M., Monribot C., Slonimski P.; Dujardin G., Kermorgant M., Monribot C., Slonimski P.; Boucherie H., Dujardin G., Kermorgant M., Monribot C., Slonimski P.; Perrot M.; Boucherie H., Dujardin G., Kermorgant M., Monribot C., Slonimski P.; RT "Two-dimensional protein map of <i>Saccharomyces cerevisiae</i> : construction of a gene-protein index.";	
RT	RT	
RT	RT	
RL	Year 11:601-613(1995).	
CC	-!- CATALYTIC ACTIVITY: ATP + 5'-phospho-D-ribosylamine + glycine --> phosphate + N(1)-[5-(phospho-D-ribosyl)glycaminide].	
CC	-!- CATALYTIC ACTIVITY: ATP + 2-(formamido)-N(1)-(5-phospho-D-ribosyl)acetamide = ADP + phosphate + 5-amino-1-(5-phospho-D-ribosyl)imidazole.	
CC	-!- PATHWAY: De novo purine biosynthesis; second step.	
CC	-!- PATHWAY: De novo purine biosynthesis; fifth step.	
CC	-!- SIMILARITY: In the N-terminal section; belongs to the GART family.	
CC	-!- SIMILARITY: In the C-terminal section; belongs to the AIR family.	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL. There are no restrictions on its use by non-profit institutions as long as its content is not removed. Usage by and modification and distribution of this statement is not removed. Usage by and entities requires a license agreement (see <a href="http://www.isb-sib.ch">http://www.isb-sib.ch</a> or send an email to license@isb-sib.ch).	
CC	EMBL: X04337; CAA27867.1; -. EMBL: Z72756; CAA96952.1; -. PIR: A26343; A26343; -. HSSP: P03178; ICLL. DR	
CC	DR GermOnline: 141283; -. SGD: S000303; ADES_7. GO: GO:0005737; C:cytoplasm; IDA. InterPro: IPR000728; AIR synth. InterPro: IPR000115; Gars. InterPro: IPR00473; PurM_cligase. DR Pfam: PF00586; AIRs; 1.	

```

DR Pfam; PF02769; AIRS_C; 1.
DR Pfam; PF01071; GARS_1;
DR Pfam; PF02842; GARS_B; 1.
DR Pfam; PF02843; GARS_C; 1.
DR Pfam; PF02844; GARS_N; 1.
DR TIGRFAMS; TIGR00877; purD; 1.
DR TIGRFAMS; TIGR00878; purM; 1.
DR PROSITE; PS00184; GARS; 1.
DR Multifunctional enzyme; Purine biosynthesis; Ligase.
KW
FT DOMAIN      1        450          GARS.
FT DOMAIN      451       802          AIRS.
SQ SEQUENCE    802 AA;   86068 MW; 1583C673E64085D2 CRC64;

```

```

Query Match          17.4%; Score 57.5; DB 1; Length 802;
Best Local Similarity 30.2%; Pred. No. 28;
Matches 19; Conservative 8; Mismatches 11; Indels 25; Gaps 3;
Qy  4 LPVFLVILLTASGPSVDA-----RLKTKDDVPLSSF----RDNAKSTLQRHQ 47
Db  94 IPVF-----GPSVKAQLEASKAFSKRPMKHNTPATSYDVFTNPEEAISFLQAH 144
Qy  48 DKS 50
Db  145 DKA 147

```

Search completed: August 10, 2004, 16:03:04  
 Job time : 13.404 secs

Blank Sheet

Result No.	Score	Query	Match	Length	DB ID	Description
1	276	83.4	64	5	Q9BPE9	Q9bpe9 conus pennula
2	196	59.2	64	5	Q9BPF1	Q9bpf1 conus pennula
3	192	58.0	63	5	Q9BPG9	Q9bp9 conus texti
4	186	56.2	61	5	Q9BH21	Q9bh21 conus texti
5	186	56.2	62	5	Q9BH86	Q9bh86 conus pennula
6	183	55.3	61	5	Q9BPF2	Q9bpf2 conus ventr
7	183	55.3	63	5	Q9BPE7	Q9bpe7 conus pennula
8	182	55.0	62	5	Q9BPG0	Q9bp90 conus pennula
9	181	54.7	64	5	Q9BPF3	Q9bpf3 conus pennula
10	180	54.4	62	5	Q9BPG8	Q9bp98 conus pennula
11	177.5	53.6	59	5	Q9BPF6	Q9bpf6 conus tessu
12	177	53.5	64	5	Q9BPF7	Q9bpf7 conus ventr
13	174.5	52.7	63	5	Q9BPF8	Q9bpf8 conus pennula
14	173	52.3	58	5	Q9BPH1	Q9bph1 conus texti
15	170.5	51.5	63	5	Q9BPF4	Q9bpf4 conus pennula
16	169.5	51.2	61	5	Q9BPF9	Q9bpf9 conus texti



		SQ	SEQUENCE	63 AA;	7163 MW;	9DF1B0FFAF2D8BA8 CRC64;					
Query Match	56.2%; Score 186; DB 5; Length 62; Best Local Similarity 69.8%; Pred. No. 7.2e-17; Matches 37; Conservative 5; Mismatches 11; Indels 0; Gaps 0;	Query Match	55.3%; Score 183; DB 5; Length 63; Best Local Similarity 69.8%; Pred. No. 1.8e-16; Matches 37; Conservative 3; Mismatches 13; Indels 0; Gaps 0;								
Qy	1 MRCLPVFVILLTASGPVDARLTKDDPFLSSFRDNAKSTLQRHQDKSVCC 53	Qy	1 MRCLPVFVILLTASGPVDARLTKDDPFLSSFRDNAKSTLQRHQDKSVCC 53								
Db	1 MRCLPVFVILLTASGPVDARLTKDDPFLSSFRDNAKSTLQRHQDKSVCC 53	Db	1 MRCLPVFVILLTASGPVDARLTKDDPFLSSFRDNAKSTLQRHQDKSVCC 53								
RESULT 6		RESULT 8		RESULT 9							
Q9BPFF2	PRELIMINARY;	Q9BPG0	PRELIMINARY;	Q9BPF3	PRELIMINARY;	SEQUENCE FROM N.A.					
ID Q9BPFF2;	PRT;	ID Q9BPG0	PRT;	ID Q9BPF3	PRT;	MEDLINE=21105969; PubMed=11158371;					
AC Q9BPFF2;	61 AA.	AC Q9BPG0;		AC Q9BPF3;							
DT 01-JUN-2001 (TREMBrel. 17, Created)		DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)		DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)							
DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)		DT 01-JUN-2003 (TREMBrel. 25, Last annotation update)		DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)							
DE Conotoxin scaffold IX.		DE Conotoxin scaffold IX.		DE Conotoxin scaffold IX.							
OS Conus ventricosus (Mediterranean cone).		OS Conus pennaceus (Feathered cone).		OS Conus pennaceus (Feathered cone).							
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda; Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda; Neogastropoda; Conoidea; Conidae; Conus.		OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda; Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda; Neogastropoda; Conoidea; Conidae; Conus.		OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda; Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda; Neogastropoda; Conoidea; Conidae; Conus.							
[1]		[1]		[1]							
RN NCBI_TaxID=117992;		RN NCBI_TaxID=37335;		RN NCBI_TaxID=37335;							
RP SEQUENCE FROM N.A.		RP SEQUENCE FROM N.A.		RP SEQUENCE FROM N.A.							
RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z., Fainzilber M.; "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";		RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z., Fainzilber M.; "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";		RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z., Fainzilber M.; "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";							
RL Mol. Biol. Evol. 18:120-131(2001).		RL Mol. Biol. Evol. 18:120-131(2001).		RL Mol. Biol. Evol. 18:120-131(2001).							
DR AF214977; AA60405; -		DR AF214969; AA60397; -		DR AF214969; AA60397; -							
GO: GO:000576; C:extracellular; IEA.		GO: GO:000576; C:extracellular; IEA.		GO: GO:000576; C:extracellular; IEA.							
GO: GO:015070; P:toxin activity; IEA.		GO: GO:015070; P:toxin activity; IEA.		GO: GO:015070; P:toxin activity; IEA.							
DR InterPro: IPR004214; Conotoxin.		DR InterPro: IPR004214; Conotoxin.		DR InterPro: IPR004214; Conotoxin.							
DR Pfam; PF02950; Conotoxin; 1.		DR Pfam; PF02950; Conotoxin; 1.		DR Pfam; PF02950; Conotoxin; 1.							
SQ SEQUENCE 61 AA; 6751 MW;		SQ SEQUENCE 62 AA; 6909 MW;		SQ SEQUENCE 62 AA; 146E5C95794E6B70 CRC64;							
Query Match	55.3%; Score 183; DB 5; Length 61; Best Local Similarity 67.9%; Pred. No. 1.8e-16; Matches 36; Conservative 7; Mismatches 10; Indels 0; Gaps 0;	Query Match	55.0%; Score 182; DB 5; Length 62; Best Local Similarity 65.6%; Pred. No. 2.4e-16; Matches 40; Conservative 3; Mismatches 16; Indels 2; Gaps 1;	Query Match	55.0%; Score 182; DB 5; Length 62; Best Local Similarity 65.6%; Pred. No. 2.4e-16; Matches 40; Conservative 3; Mismatches 16; Indels 2; Gaps 1;	Query Match	55.0%; Score 182; DB 5; Length 62; Best Local Similarity 65.6%; Pred. No. 2.4e-16; Matches 40; Conservative 3; Mismatches 16; Indels 2; Gaps 1;	Query Match	55.0%; Score 182; DB 5; Length 62; Best Local Similarity 65.6%; Pred. No. 2.4e-16; Matches 40; Conservative 3; Mismatches 16; Indels 2; Gaps 1;	Query Match	55.0%; Score 182; DB 5; Length 62; Best Local Similarity 65.6%; Pred. No. 2.4e-16; Matches 40; Conservative 3; Mismatches 16; Indels 2; Gaps 1;
Qy 1 MRCLPVFVILLTASGPVDARLTKDDPFLSSFRDNAKSTLQRHQDKSVCC 53		Qy 1 MRCLPVFVILLTASGPVDARLTKDDPFLSSFRDNAKSTLQRHQDKSVCC 53		Qy 1 MRCLPVFVILLTASGPVDARLTKDDPFLSSFRDNAKSTLQRHQDKSVCC 53							
Db 1 MRCLPVFVILLTASGPVDARLTKDDPFLSSFRDNAKSTLQRHQDKSVCC 53		Db 1 MRCLPVFVILLTASGPVDARLTKDDPFLSSFRDNAKSTLQRHQDKSVCC 53		Db 1 MRCLPVFVILLTASGPVDARLTKDDPFLSSFRDNAKSTLQRHQDKSVCC 53							
RESULT 7		RESULT 7		RESULT 7		SEQUENCE FROM N.A.					
Q9BPET7	PRELIMINARY;	Q9BPET7	PRELIMINARY;	Q9BPET7	PRELIMINARY;	MEDLINE=21105969; PubMed=11158371;					
ID Q9BPET7;	PRT;	ID Q9BPET7;	PRT;	ID Q9BPET7;	PRT;						
AC Q9BPET7;	63 AA.	AC Q9BPET7;	63 AA.	AC Q9BPET7;	63 AA.						
DT 01-JUN-2001 (TREMBrel. 17, Created)		DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)		DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)							
DT 01-JUN-2001 (TREMBrel. 17, Last sequence update)		DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)		DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)							
DE Conotoxin scaffold IX.		DE Conotoxin scaffold IX.		DE Conotoxin scaffold IX.							
OS Conus pennaceus (Feathered cone).		OS Conus pennaceus (Feathered cone).		OS Conus pennaceus (Feathered cone).							
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda; Neogastropoda; Conoidea; Conidae; Conus.		OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda; Neogastropoda; Conoidea; Conidae; Conus.		OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda; Neogastropoda; Conoidea; Conidae; Conus.							
[1]		[1]		[1]							
RN NCBI_TaxID=37335;		RN NCBI_TaxID=37335;		RN NCBI_TaxID=37335;							
RP SEQUENCE FROM N.A.		RP SEQUENCE FROM N.A.		RP SEQUENCE FROM N.A.							
RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z., Fainzilber M.; "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";		RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z., Fainzilber M.; "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";		RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z., Fainzilber M.; "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";							
RL Mol. Biol. Evol. 18:120-131(2001).		RL Mol. Biol. Evol. 18:120-131(2001).		RL Mol. Biol. Evol. 18:120-131(2001).							
DR GO:0005576; C:extracellular; IEA.		DR GO:0005576; C:extracellular; IEA.		DR GO:0005576; C:extracellular; IEA.							
DR GO: GO:009405; P:pathogenesis; IEA.		DR GO: GO:009405; P:pathogenesis; IEA.		DR GO: GO:009405; P:pathogenesis; IEA.							
DR InterPro: IPR004214; Conotoxin.		DR InterPro: IPR004214; Conotoxin.		DR InterPro: IPR004214; Conotoxin.							
DR Pfam; PF02950; Conotoxin; 1.		DR Pfam; PF02950; Conotoxin; 1.		DR Pfam; PF02950; Conotoxin; 1.							
Qy 59 F 59		Qy 61 F 61		Qy 61 F 61							

DR GO; GO:0005576; C: extracellular; IEA.  
 DR GO; GO:0015070; F: toxin activity; IEA.  
 DR GO; GO:009405; P: pathogenesis; IEA.  
 DR InterPro; IPR004214; Conotoxin.  
 DR Pfam; PF02950; Conotoxin; 1.  
 SEQUENCE 64 AA; 7146 MW; 5E5A04C6B6ADDFF88 CRC64;

Query Match 54.7%; Score 181; DB 5; Length 64;  
 Best Local Similarity 62.3%; Pred. No. 3.e-16; Indels 2; Gaps 1;  
 Matches 40; Conservative 3; Mismatches 19; Indels 2; Gaps 1;  
 AC 1 MRCLPFPVILLIITASGPSPYDARLKTQDKSVC--GYKLC 58  
 Db 1 MCCLPFPVILLIITASGPSPYDARLKTQDKSVC--GYKLC 60

RESULT 10  
 Q9BPG8 PRELIMINARY; PRT; 62 AA.  
 ID Q9BPG8  
 AC Q9BPG8  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DE Conotoxin scaffold IX.  
 OS Conus pennaceus (Feathered cone).  
 OC Apogastropoda; Mollusca; Gastropoda; Orthogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.  
 OX NCBI\_TAXID=37335;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=21105969;  
 RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,  
 RA Painzilber M.;  
 RA "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";  
 RA "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";  
 RA MOL. BIOL. EVOL. 18:120-131(2001).  
 DR EMBL; AF214960; MAG60388\_1;  
 DR GO; GO:0005576; C: extracellular; IEA.  
 DR GO; GO:0015070; F: toxin activity; IEA.  
 DR GO; GO:009405; P: pathogenesis; IEA.  
 DR InterPro; IPR004214; Conotoxin.  
 DR Pfam; PF02950; Conotoxin; 1.  
 SEQUENCE 62 AA; 6969 MW; 0DA718B0BDFA9ED1 CRC64;

Query Match 54.4%; Score 180; DB 5; Length 62;  
 Best Local Similarity 59.7%; Pred. No. 4.e-16; Indels 0; Gaps 0;  
 Matches 37; Conservative 5; Mismatches 20; Indels 0; Gaps 0;

QY 1 MRCLPFPVILLIITASGPSPYDARLKTQDKSVC--GYKLC 60  
 DB 1 MRCLPFPVILLIITASGPSPYDARLKTQDKSVC--GYKLC 60

RESULT 11  
 Q9BPF6 PRELIMINARY; PRT; 59 AA.  
 ID Q9BPF6  
 AC Q9BPF6  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Conotoxin scaffold IX.  
 OS Conus tessulatus.  
 OC Apogastropoda; Mollusca; Gastropoda; Orthogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.

OX NCBI\_TAXID=101317;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX PubMed=11158371;  
 RA Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z.,  
 RA Painzilber M.;  
 RA "Mechanisms for Evolving Hypervariability: The Case of Conopeptides.";  
 RA MOL. BIOL. EVOL. 18:120-131(2001).  
 DR EMBL; AF214972; MAG60400\_1;  
 DR GO; GO:0005576; C: extracellular; IEA.  
 DR GO; GO:0016030; C: membrane; IEA.  
 DR GO; GO:0008233; F: peptidase activity; IEA.  
 DR GO; GO:0009405; P: pathogenesis; IEA.  
 DR InterPro; IPR004214; Conotoxin.  
 DR Pfam; PF02950; Conotoxin; 1.  
 DR PROSITE; PS00761; SPASE\_1\_3; 1.  
 SQ SEQUENCE 64 AA; 6982 MW; 856B912BA210ABC CRC64;

Query Match 53.5%; Score 177; DB 5; Length 64;  
 Best Local Similarity 65.6%; Pred. No. 1.e-15; Indels 2; Gaps 2;  
 Matches 42; Conservative 3; Mismatches 17; Indels 2; Gaps 2;

QY 1 MRCLPFPVILLIITASGPSPYDARLKTQDKSVC--GYKLC 58  
 DB 1 MRCLPFPVILLIITASGPSPYDARLKTQDKSVC--GYKLC 60

RESULT 13  
 Q9BPF8  
 ID Q9BPF8  
 AC Q9BPF8  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Conotoxin scaffold IX.  
 OS Conus tessulatus.  
 OC Apogastropoda; Mollusca; Gastropoda; Orthogastropoda;  
 OC Neogastropoda; Conoidea; Conidae; Conus.

ID	Q9BBF8	PRELIMINARY;	PRT;	63 AA.	Best Local Similarity 65.0%; Pred. No. 3.5e-15; Matches 39; Conservative 3; Mismatches 12; Indels 6; Gaps 2;
AC	Q9BBF8				
DT	01-JUN-2001 (TREMBLrel. 17, Created)				
DT	01-JUN-2001 (TREMBLrel. 17, Last sequence update)				
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)				
DE	Conotoxin scaffold IX.				
OS	Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda; Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda; Neogastropoda; Conoidea; Conidae; Conus.				
OC					
OX					
[1]	NCBI_TaxID=37335;				
RN					
RP	SEQUENCE FROM N.A. MEDLINE=21105969; PubMed=11158371;				
RX					
RA	Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z., Fainzilber M.; "Mechanisms for Evolving Hypervariability: The Case of Conopeptides."; Mol. Biol. Evol. 18:120-131(2001).				
RL	GO: GO:0005576; C:extracellular; IEA.				
DR	GO: GO:0015070; P:toxin activity; IEA.				
DR	GO: GO:0009405; P:pathogenesis; IEA.				
DR	InterPro: IPR004214; Conotoxin.				
DR	Pfam: PF02950; Conotoxin_1.				
SQ	SEQUENCE 63 AA; 6878 MW; 27DD9A64D056B548 CRC64;				
Query Match	52.7%; Score 174.5%; DB 5; Length 63;				
Best Local Similarity 60.3%; Pred. No. 2.4e-15;	Mismatches 38; Conservative 7; Indels 1; Gaps 1;				
Matches					
Qy	1 MRCLPVVILLITASGRPSVDAIRLTKDDVPLSSFRDNAKSTLQRHDKSVCC-GYKLCP 59				
Db	1 MHCLSVVILLITASAPSVDQPKEDDVPSFHDDQVRLDIRMCLGTSGCC 60				
Qy	60 PCG 62				
Db	61 PWG 63				
Query Match	51.5%; Score 170.5%; DB 5; Length 63;				
Best Local Similarity 55.6%; Pred. No. 8.2e-15;	Matches 35; Conservative 8; Mismatches 19; Indels 1; Gaps 1;				
Matches					
Q9BPH1	PRELIMINARY;	PRT;	58 AA.		
ID	Q9BPH1				
AC	Q9BPH1				
DT	01-JUN-2001 (TREMBLrel. 17, Created)				
DT	01-OCT-2003 (TREMBLrel. 25, Last sequence update)				
DE	Conotoxin scaffold IX.				
OS	Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda; Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda; Neogastropoda; Conoidea; Conidae; Conus.				
OC					
OX					
[1]	NCBI_TaxID=6434;				
RN					
RP	SEQUENCE FROM N.A. MEDLINE=21105669; PubMed=11158371;				
RA	Conticello S.G., Gilad Y., Avidan N., Ben-Asher E., Levy Z., Fainzilber M.; "Mechanisms for Evolving Hypervariability: The Case of Conopeptides."; Mol. Biol. Evol. 18:120-131(2001).				
RL	GO; GO:0005576; C:extracellular; IEA.				
DR	GO; GO:0005509; P:calcium ion binding; IEA.				
DR	GO; GO:0015070; P:lipid catabolism; IEA.				
DR	GO; GO:0016042; P:phospholipase A2 activity; IEA.				
DR	InterPro: IPR004214; Conotoxin.				
DR	Pfam: PF01212; PhospholipaseA2.				
DR	PROSITE: PS00118; PA2_HIS; 1.				
SQ	SEQUENCE 58 AA; 6563 MW; D8B7537B6B516BBA CRC64;				
Query Match	52.3%; Score 173; DB 5; Length 58;				

Search completed: August 10, 2004, 16:04:22  
Job time : 57.1351 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

4 protein - protein search, using sw model  
run on: August 10, 2004, 15:55:40 ; Search time 15.5676 Seconds  
(without alignments)  
217.797 Million cell updates/sec

title:	US-10-072-602B-534					
perfect score:	79					
sequence:	1 SVCCGGYKLCPFC 12					
scoring table:	BLOSUM62					
	Gapop 10.0 , Gapext 0.5					
searched:	1586107 seqs, 282547505 residues					
total number of hits satisfying chosen parameters:	1586107					
st-processing: Minimum Match 0% Maximum Match 100%						
Listing first 45 summaries						
database :						
A_Geneseq_29Jan04:*						
1: geneseqP1980s:*						
2: geneseqP1990s:*						
3: GeneseqP2000s:*						
4: geneseqP2001s:*						
5: geneseqP2002s:*						
6: geneseqP2003as:*						
7: geneseqP2003bs:*						
8: geneseqP2004s:*						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
%	Query	Match	Length			
built	No.	Score	DB	ID	Description	
1	79	100.0	12	5	ABG99749	Corus sp
2	79	100.0	62	5	ABG99600	Corus sp
3	69	87.3	13	5	ABG99744	Corus sp
4	69	87.3	61	5	ABG99585	Corus sp
5	68	86.1	12	3	AAB08018	Amino aci
6	68	86.1	13	3	AAV92229	Aay92229 Chi-conot
7	68	86.1	13	3	AAV92210	Aay92230 Chi-conot
8	68	86.1	13	3	AAB08017	Aab08017 Amino aci
9	68	86.1	61	3	AAV92231	Aay92231 Chi-conot
10	68	86.1	61	3	AAB08016	Aab08016 Amino aci
11	68	86.1	61	5	ABG99595	Corus sp
12	63	79.7	11	5	ABG99748	Abg99748 Corus sp
13	63	79.7	11	5	ABG99739	Abg99739 Corus sp
14	63	79.7	12	5	ABG99743	Abg99743 Corus sp
15	63	79.7	12	5	ABG99742	Abg99742 Corus sp
16	63	79.7	13	5	ABG99741	Abg99741 Corus sp
17	63	79.7	13	5	ABG99753	Abg99753 Corus sp
18	63	79.7	13	5	ABG99740	Abg99740 Corus sp
19	63	79.7	13	5	ABG99750	Abg99750 Corus sp
20	63	79.7	16	5	ABG99602	Abg99602 Corus sp
21	63	79.7	61	5	ABG99400	Abg99400 Corus sp
22	63	79.7	61	5	ABG99598	Abg99598 Corus sp
23	63	79.7	62	5	ABG99591	Abg99591 Corus sp
24	63	79.7	64	5	ABG99470	Abg99470 Corus sp
25	63	79.7	64	5	ABG99587	Abg99587 Corus sp

63	79.7	64	5	ABG99608	Conus sp
62	79.7	64	5	ABG99593	Conus sp
62	78.5	12	3	AAB08019	Amino aci
62	78.5	12	5	ABG99601	Conus sp
62	74.7	12	5	ABG99747	Conus sp
62	74.7	12	5	ABG99747	Conus sp
62	74.7	12	5	ABG99738	Conus sp
62	74.7	12	5	ABG99751	Conus sp
62	74.7	13	5	ABG99746	Conus sp
62	74.7	13	5	ABG99746	Conus sp
62	74.7	62	5	ABG99517	Conus sp
62	74.7	62	5	ABG99604	Conus sp
62	73.4	12	5	ABG99752	Conus sp
62	73.4	12	5	ABG99606	Conus sp
62	73.4	12	5	ABG99754	Conus sp
62	73.4	14	5	ABG99754	Conus sp
62	69.6	16	5	ABG99610	Conus sp
62	68.4	12	3	AAB08014	Aab08014
62	68.4	12	3	AAB08015	Generic f
62	68.4	12	5	ABG99592	Conus sp
62	68.4	13	3	AAB08013	Generic f
62	68.4	13	5	ABG99588	Conus sp
62	68.4	13	5	ABG99471	Conus sp
ALIGNMENTS					
174_9					
ABG99749 standard; peptide; 12 AA.					
ABG99749;					
117-JAN-2003 (first entry)					
Conus sp conotoxin-associated peptide SEQ ID 534.					
Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator; ligand-gated ion channel modulator; pain-relief.					
Conus aulicus.					
WO200264740-A2.					
22-AUG-2002.					
111-FEB-2002; 2002WO-US003887.					
09-FEB-2001; 2001US-0267408P.					
(COGN-) COGNETIX INC. (UTAH ) UNIV UTAH RES FOUND.					
Dolivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ, Grillley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM; NMPITI; 2002-706921/76.					
New cone snail conotoxin peptides, useful as a pain reliever for alleviating pain in an individual suffering from pain or who is about to be subjected to a pain-causing event, or for treating voltage-gated ion channel disorders.					
Claim 1; Page 287; 305pp; English.					
This invention describes novel conotoxin peptides from the cone snail, Conus which have analgesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders. The radiolabelled conotoxin peptide is also useful for					

screening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters. ABG99360-ABG99853 represent the conotoxin protein and peptides described in the disclosure of the invention						
SQ	Sequence 12 AA;	RESULT 2	Query Match ID ABG99600	Score 79; DB 5; Length 12;	Best Local Similarity 100.0%;	Pred. No. 0.00022;
XX			XX	Mismatches 0;	Indels 0;	Gaps 0;
XX			AC			
XX			ABG99600;			
XX			XX			
DT	17-JAN-2003	(first entry)	DE			
XX			DE			
XX			XX			
KW	Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;		XX			
KW	1-ligand-gated ion channel modulator; pain-relief.		XX			
XX			OS			
OS	Conus aulicus.		XX			
XX			PN			
XX			PN	WO200264740-A2.		
XX			PD	22-AUG-2002.		
XX			PP	11-FEB-2002; 2002WO-US003887.		
XX			XX			
PR	09-FEB-2001; 2001US-0267408P.		XX			
XX			PA	(COGN-) COGNETIX INC.		
PA	(UTAH ) UNIV UTAH RES FOUND.		XX			
PA			PI	Olivera BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ;		
PA			PI	Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;		
PA			XX			
DR	WPI: 2002-706921/76.		DR	N-PSDB; ABX04337.		
XX			XX	New cone snail conotoxin peptides, useful as a pain reliever for alleviating pain in an individual suffering from pain or who is about to be subjected to a pain-causing event, or for treating voltage-gated ion channel disorders.		
XX			XX	Claim 1; Page 239; 305pp; English.		
XX			XX	This invention describes novel conotoxin peptides from the cone snail, genus Conus which have analgesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders, ligand-gated ion channel disorders or receptor disorders. The radio-labelled conotoxin peptide is also useful for characterising a new site on these receptors or channels, and for screening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters ABG99360-ABG99853 represent the conotoxin protein and peptides described in the disclosure of the invention		
XX			XX	Sequence 62 AA;		
SQ			SQ	Score 100.0%; DB 5; Length 62;		
Query Match			Query Match			

ABG99585  
 ID ABG99585 standard; protein; 61 AA.  
 XX  
 AC ABG99585;  
 XX  
 DT 17-JAN-2003 (first entry)  
 XX  
 Conus sp conotoxin-associated protein SEQ ID 330.  
 XX  
 Conotoxin; cone snail; analgesic; voltage-gated ion channel modulator;  
 ligand-gated ion channel modulator; pain-relief.  
 XX  
 Conus marmoreus.  
 XX  
 WO200264740-A2.  
 XX  
 PD 22-AUG-2002.  
 XX  
 PP 11-FEB-2002; 2002WO-US003887.  
 XX  
 PR 09-FEB-2001; 2001US-0267408B.  
 XX  
 PA (COGNITIX INC.  
 (UTAH ) UNIV UTAH RES FOUND.  
 XX  
 PI Oliveira BM, McIntosh JM, Watkins M, Garrett JE, Cruz LJ,  
 Grilley M, Walker CS, Shetty R, Jones RM, Schoenfeld RM;  
 DR 2002-706921/76.  
 DR N-PSDB; ABX04930.  
 XX  
 New cone snail conotoxin peptides, useful as a pain reliever for  
 alleviating pain in an individual suffering from pain or who is about to  
 be subjected to a pain-causing event, or for treating voltage-gated ion  
 channel disorders.  
 XX  
 PS Claim 1; Page 231; 305pp; English.  
 XX  
 This invention describes novel conotoxin peptides from the cone snail  
 genus Conus which have analgesic activity and can act as a voltage-gated  
 ion channel modulator or a ligand-gated ion channel modulator. The  
 conotoxin peptide is useful as a pain-relieving agent for alleviating  
 pain in an individual who is either exhibiting pain or is about to be  
 subjected to a pain-causing event. The conotoxin peptide is also useful  
 for treating or preventing disorders associated with voltage-gated ion  
 channel disorders. The radiolabeled conotoxin peptide is also useful for  
 characterising a new site on these receptors or channels, and for  
 screening and identifying novel small molecules that interact with the  
 above-mentioned channels or receptors, which are monoamine transporters.  
 CC ABG99360-ABG99853 represent the conotoxin protein and peptides described  
 in the disclosure of the invention  
 XX  
 Sequence 61 AA;  
 XX  
 Query Match 87.3%; Score 69; DB 5; Length 61;  
 Best Local Similarity 90.9%; Pred. No. 0.021;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 YY 2 VCCGYKLCPFC 12  
 Db 51 VCCGYKLCPFC 61  
 XX  
 RESULT 5  
 AAB08018  
 ID AAB08018 standard; peptide; 12 AA.  
 XX  
 AC AAB08018;  
 XX  
 DT 14-NOV-2000 (first entry)  
 XX  
 DE Amino acid sequence of the conotoxin peptide Mar2.

XX  
 KW Ap-conotoxin; conotoxin; venom; cone snail; analgesic; pain; Mar2.  
 XX  
 OS Conus marmoreus.  
 XX  
 FH Key  
 FT Modified-site 12  
 /note= "hydroxy-Pro"  
 XX  
 WO20044769-A1.  
 XX  
 PD 03-AUG-2000.  
 XX  
 PP 28-JAN-2000; 2000WO-US001978.  
 XX  
 PR 29-JAN-1999; 99US-0118381P.  
 PR 28-DEC-1999; 99US-0173343P.  
 XX  
 PA (UTAH ) UNIV UTAH RES FOUND.  
 XX  
 PI McIntosh JM, Oliveira BM, Cruz LJ;  
 XX  
 DR WPI; 2000-47622/41.  
 XX  
 PT Purified ap-conotoxin derived from cone snail venom for use as an  
 analgesic.  
 XX  
 PS Claim 14; Page: 29pp; English.  
 XX  
 CC The present sequence represents an ap-conotoxin peptide, designated Mar2.  
 CC Conotoxins are naturally available in minute amounts in the venom of cone  
 CC snails. The peptides have analgesic activity. The peptides are used to  
 CC treat or prevent pain. note: this sequence does not appear in the  
 CC specification; it was created using information provided  
 XX  
 SQ Sequence 12 AA;

Query Match 86.1%; Score 68; DB 3; Length 12;  
 Best Local Similarity 90.9%; Pred. No. 0.0072;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 YY 2 VCCGYKLCPFC 12  
 Db 2 VCCGYKLCPFC 12  
 AC AAY92229;  
 XX  
 RESULT 6  
 AAY92229 standard; peptide; 13 AA.  
 ID AAY92229  
 XX  
 DB Chi-conotoxin peptide, chi-MrIA.  
 XX  
 KW chi-conotoxin; Chi MrIA; cone snail; inhibitor; amine transporter;  
 KW neuronal; noradrenaline transporter; urinary tract disorder; analgesic;  
 KW antiarrhythmic; cardiotonic; antidepressant; anxiolytic; anti-inflammatory.  
 XX  
 OS Conus marmoreus.  
 XX  
 FH Key  
 FT Misc-difference 12  
 /label= "4Hyp  
 /note= "4-hydroxyproline"  
 XX  
 WO20020444-A1.  
 XX  
 PD 13-APR-2000.  
 XX  
 PF 01-OCT-1999;  
 XX

PR 02-OCT-1998; 98AU-00006274.  
 XX PA (UYQU ) UNIV QUEENSLAND.  
 XX PI Lewis RJ, Alewood PF, Sharpe IA;  
 XX DR WPI; 2000-303738/26.

XX Isolated, synthetic or recombinant chi-conotoxin peptide capable of inhibiting neuronal amine transporter used for treatment or prophylaxis of urinary or cardiovascular conditions, mood disorders, or treatment/control of pain/inflammation.  
 XX PS Claim 3; Page 33; 47pp; English.

XX This conotoxin, chi-MrIA, is a member of a new class of conotoxins, designated chi-conotoxin. It was isolated from the venom of the mollusc hunting cone snail, Conus marmoreus. The peptide is an inhibitor of the neuronal amine transporters, especially the neuronal noradrenaline transporter. Inhibitors of noradrenaline re-uptake which have a negligible anti-cholinergic effect are particularly useful in the treatment of lower urinary tract disorders. Chi-MrIA (0.1 nM-1 micro M) inhibited the accumulation of radiolabeled noradrenalin in a concentration-dependent manner, with a log IC-50 value of -8.17 plus or minus 0.0275 (n = 4). The concentration of chi-MrIA required to inhibit the accumulation by 50 percent was found to be approximately 7 nM. This concentration is approximately one order of magnitude lower than that needed for desipramine to produce the same effect. The peptides are useful for the treatment or prophylaxis of urinary or cardiovascular conditions or diseases (arrhythmia or coronary heart failure) or mood disorders (depression, anxiety or cravings), or the treatment or control of pain or inflammation (chronic pain, neuropathic pain or inflammatory pain)  
 XX SQ Sequence 13 AA;  
 XX Query Match Score 68; DB 3; Length 13;  
 XX Best Local Similarity Pred. No. 0.0077;  
 XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX QY 2 VCCGYKLCPBC 12  
 XX 3 VCCGYKLCPBC 13  
 XX Db

RESULT 7  
 ID AAT92230  
 ID AAY92230 standard; peptide; 13 AA.  
 XX AC AAY92230;  
 XX DT 10-AUG-2000 (first entry)  
 XX DE Chi-conotoxin peptide, chi-MrIB.  
 XX KW chi-conotoxin; chi-MrIB; cone snail; inhibitor; amine transporter;  
 KW neuronal; noradrenaline transporter; urinary tract disorder; analgesic;  
 KW antiarrhythmic; cardiant; antidepressant; antiholytic; anti-inflammatory.  
 XX OS Conus marmoreus.  
 XX EH Key  
 FT Misc-difference 12  
 FT /label= "4Hyp  
 FT /note= "4-hydroxyproline"  
 XX FN WO200002044-A1.  
 XX ED 13-APR-2000.  
 XX PP 01-OCT-1999;  
 XX PR 02-OCT-1998;  
 XX PA (UYQU ) UNIV QUEENSLAND.  
 XX PI Lewis RJ, Alewood PF, Sharpe IA;  
 XX DR WPI; 2000-303738/26.

XX Isolated, synthetic or recombinant chi-conotoxin used for treatment or prophylaxis of urinary or cardiovascular conditions, mood disorders, or treatment/control of pain/inflammation.  
 XX PS Claim 3; Page 33; 47pp; English.

XX This conotoxin, chi-MrIB, is a member of a new class of conotoxins, CC hunting cone snail, Conus marmoreus. The peptide is an inhibitor of the neuronal amine transporters, especially the neuronal noradrenaline transporter. Inhibitors of noradrenaline re-uptake which have a negligible anti-cholinergic effect are particularly useful in the treatment of lower urinary tract disorders. Chi-MrIA (0.1 nM-1 micro M) inhibited the accumulation of radiolabeled noradrenalin in a concentration-dependent manner, with a log IC-50 value of -8.17 plus or minus 0.0275 (n = 4). The concentration of chi-MrIA required to inhibit the accumulation by 50 percent was found to be approximately 7 nM. This concentration is approximately one order of magnitude lower than that needed for desipramine to produce the same effect. The peptides are useful for the treatment or prophylaxis of urinary or cardiovascular conditions or diseases (arrhythmia or coronary heart failure) or mood disorders (depression, anxiety or cravings), or the treatment or control of pain or inflammation (chronic pain, neuropathic pain or inflammatory pain)  
 XX SQ Sequence 13 AA;  
 XX Query Match Score 86.1%; DB 3; Length 13;  
 XX Best Local Similarity Pred. No. 0.0077;  
 XX Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 XX QY 2 VCCGYKLCPBC 12  
 XX 3 VCCGYKLCPBC 13  
 XX Db

RESULT 8  
 ID AAB08017  
 ID AAB08017 standard; peptide; 13 AA.  
 XX AC AAB08017;  
 XX DT 14-NOV-2000 (first entry)  
 XX DE Amino acid sequence of the conotoxin peptide Marl.  
 XX KW Ap-conotoxin; conotoxin; venom; cone snail; analgesic; pain; Marl.  
 XX OS Conus marmoreus.  
 XX FH Key  
 FT Modified-site 12  
 FT /note= "hydroxy-Pro"  
 XX PN WO200044769-A1.  
 XX PD 03-AUG-2000.  
 XX PP 28-JAN-2000; 2000WO-US001978.  
 XX PR 29-JAN-1999;  
 XX PR 28-DEC-1999;  
 XX PA (UTAH ) UNIV UTAH RES FOUND.  
 XX

PI McIntosh JM, Olivera BM, Cruz LJ;  
 XX WPI: 2000-476222/41.  
 Purified ap-conotoxin derived from cone snail venom for use as an  
 analgesic.  
 PT Claim 13; Page; 29pp; English.  
 XX The present sequence represents an ap-conotoxin Peptide, designated Mari. 1.  
 Conotoxins are naturally available in minute amounts in the venom of cone  
 snails. The peptides have analgesic activity. The peptides are used to  
 treat or prevent pain. note: this sequence does not appear in the  
 specification; it was created using information provided  
 XX Sequence 13 AA;  
 Query Match 86.1%; Score 68; DB 3; Length 13;  
 Best Local Similarity 90.9%; Pred. No. 0.0077; Indels 0; Gaps 0;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 SQ

RESULT 9  
 AAY92231 standard; protein; 61 AA.  
 XX AAY92231;  
 AC DT 10-AUG-2000 (first entry)  
 XX DE Chi-conotoxin, chi-MRIA, leader and mature peptide.  
 KW chi-conotoxin; chi-MRIA; cone snail; inhibitor; amine transporter;  
 neuronal; noradrenalin transporter; urinary tract; analgesic; cardiotonic;  
 antiarrhythmic; antidepressant; anxiolytic; anti-inflammatory.  
 KW Conus marmoreus.  
 XX OS WO200020444-A1.  
 PN PR 01-OCT-1999; 99US-011881P.  
 XX DR 02-OCT-1998; 98AU-00006274.  
 PD PR 13-APR-2000.  
 XX PA (UTAH ) UNIV UTAH RBS FOUND.  
 PP PI McIntosh JM, Olivera BM, Cruz LJ,  
 XX PR DR WPI; 2000-476222/41.  
 XX N-PSDB; AAA633513.  
 PA PS Purified ap-conotoxin derived from cone snail venom for use as an  
 analgesic.  
 XX PS Claim 23; Page 13-14; 29pp; English.  
 XX DR WPI; 2000-303738/26.  
 DR N-PSDB; AAA09112.  
 PA PS Isolated, synthetic or recombinant chi-conotoxin peptide capable of  
 PT inhibiting neuronal amine transporters used for treatment or prophylaxis  
 PT of urinary cardiovascular conditions, mood disorders, or  
 PT treatment/control of pain/inflammation.  
 XX Example 7; Page 31; 47pp; English.  
 XX This sequence is the conotoxin, chi-MRIA, a member of a new class of  
 CC conotoxins, designated chi-conotoxin. It was isolated from the venom of  
 CC the mollusc hunting cone snail, Conus marmoreus. The peptide is an  
 CC inhibitor of the neuronal amine transporters, especially the neuronal  
 CC norepinephrine transporter. Inhibitors of norepinephrine re-uptake which  
 CC have a negligible anti-cholinergic effect are particularly useful in the  
 CC treatment of lower urinary tract disorders. Chi-MRIA (0.1 μM-1 micro M)  
 CC inhibited the accumulation of radiolabelled norepinephrine in a  
 CC concentration-dependent manner, with a log IC-50 value of -8.17 plus or

PI McIntosh JM, Olivera BM, Cruz LJ;  
 XX WPI: 2000-476222/41.  
 Purified ap-conotoxin derived from cone snail venom for use as an  
 analgesic.  
 PT Claim 13; Page; 29pp; English.  
 XX The concentration of chi-MRIA required to inhibit  
 CC the accumulation by 50 percent was found to be approximately 7 μM. This  
 CC concentration is approximately one order of magnitude lower than that  
 CC needed for desipramine to produce the same effect. The peptides are  
 CC useful for the treatment or prophylaxis of urinary or cardiovascular  
 CC conditions or diseases (arrhythmia or coronary heart failure) or mood  
 CC disorders (depression, anxiety or cravings), or the treatment or control  
 CC of pain or inflammation (chronic pain, neuropathic pain or inflammatory  
 CC pain).  
 XX Sequence 61 AA;  
 Query Match 86.1%; Score 68; DB 3; Length 61;  
 Best Local Similarity 90.9%; Pred. No. 0.028;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 SQ

RESULT 10  
 AAB08016 standard; protein; 61 AA.  
 ID AAB08016  
 XX AC AAB08016;  
 AC DT 14-NOV-2000 (first entry)  
 XX DE Amino acid sequence of the conotoxin Mari propeptide.  
 KW Ap-conotoxin; conotoxin; venom; cone snail; analgesic; pain; Mari.  
 KW Conus marmoreus.  
 OS XX WO200044769-A1.  
 PN PR 03-AUG-2000.  
 XX PD 28-JAN-2000; 2000WO-US001978.  
 XX PR 29-JAN-1999; 99US-011881P.  
 PR 28-DEC-1999; 99US-017343P.  
 XX DR (UTAH ) UNIV UTAH RBS FOUND.  
 PA PR PA  
 XX PI McIntosh JM, Olivera BM, Cruz LJ,  
 XX DR WPI; 2000-476222/41.  
 N-PSDB; AAA633513.  
 XX PS Purified ap-conotoxin derived from cone snail venom for use as an  
 analgesic.  
 XX PS Claim 23; Page 13-14; 29pp; English.  
 XX DR WPI; 2000-303738/26.  
 DR N-PSDB; AAA09112.  
 PA PS Isolated sequence represents a Mari propeptide. Mari is an ap-  
 CC conotoxin peptide. Conotoxins are naturally available in minute amounts  
 CC in the venom of cone snails. The peptides have analgesic activity. The  
 CC peptides are used to treat or prevent pain  
 XX Sequence 61 AA;  
 Query Match 86.1%; Score 68; DB 3; Length 61;  
 Best Local Similarity 90.9%; Pred. No. 0.028;  
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 SQ

RESULT 11  
 VCCGYKLCPG 12  
 51 VCCGYKLCPG 61





PS Claim 1; Page 286; 305pp; English.

XX This invention describes novel conotoxin peptides from the cone snail, Conus which have analgesic activity and can act as a voltage-gated ion channel modulator or a ligand-gated ion channel modulator. The conotoxin peptide is useful as a pain-relieving agent for alleviating pain in an individual who is either exhibiting pain or is about to be subjected to a pain-causing event. The conotoxin peptide is also useful for treating or preventing disorders associated with voltage-gated ion channel disorders, ligand-gated ion channel disorders or receptor disorders. The radiolabeled conotoxin peptide is also useful for characterising a new site on these receptors or channels, and for screening and identifying novel small molecules that interact with the above-mentioned channels or receptors, which are monoamine transporters. ABG930-ABG983 represent the conotoxin protein and peptides described in the disclosure of the invention

XX Sequence 12 AA;

Query Match Score 63; DB 5; Length 12;  
Best Local Similarity 79.7%; Pred. No. 0.035;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SVCCGYKLCFPC 12  
| || : | | |  
1 STCCGFNCRPC 12

Search completed: August 10, 2004, 16:02:37  
Job time : 15.5676 SECs

GenCore version 5.1.6  
 Copyright (c) 1993 - 2004 Compugen Ltd.

## OM protein - Protein search, using sw model

Run on: August 10, 2004, 16:00:55 ; Search time 4.7027 seconds  
 (without alignments)  
 131.735 Million cell updates/sec

Title: US-10-072-602B-534

Perfect score: 79  
 Sequence: 1 SVCCGYKLCFPC 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51623971 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

- 1: /cgri2\_6.ptodata/2/iaa/5A\_COMB.pep:\*
- 2: /cgri2\_6.ptodata/2/iaa/5B\_COMB.pep:\*
- 3: /cgri2\_6.ptodata/2/iaa/6A\_COMB.pep:\*
- 4: /cgri2\_6.ptodata/2/iaa/6B\_COMB.pep:\*
- 5: /cgri2\_6.ptodata/2/iaa/PETUS\_COMB.pep:\*
- 6: /cgri2\_6.ptodata/2/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	45	57.0	56	4	US-09-336-536-65	Sequence 65, App1
2	45	57.0	187	4	US-09-336-536-65	Sequence 60, App1
3	45	57.0	213	4	US-09-336-536-58	Sequence 58, App1
4	44	55.7	503	4	US-09-914-559-13	Sequence 13, App1
5	43.5	55.1	38	1	US-08-137-00-29	Sequence 29, App1
6	43.5	55.1	38	1	US-08-177-383-29	Sequence 29, App1
7	43.5	55.1	38	1	US-08-487-174-29	Sequence 29, App1
8	43.5	55.1	38	1	US-08-480-550-29	Sequence 29, App1
9	43.5	55.1	42	1	US-08-477-383-59	Sequence 59, App1
10	43.5	55.1	42	1	US-08-487-174-59	Sequence 59, App1
11	43.5	55.1	42	1	US-08-480-550-59	Sequence 59, App1
12	43.5	55.1	80	1	US-08-137-00-44	Sequence 44, App1
13	43.5	55.1	80	1	US-08-477-383-44	Sequence 44, App1
14	43.5	55.1	80	1	US-08-487-174-44	Sequence 44, App1
15	43.5	55.1	80	1	US-08-480-750-44	Sequence 44, App1
16	42.5	53.8	30	1	US-08-137-800-35	Sequence 35, App1
17	42.5	53.8	30	1	US-08-477-183-35	Sequence 35, App1
18	42.5	53.8	30	1	US-08-487-174-35	Sequence 35, App1
19	42.5	53.8	30	1	US-08-137-900-27	Sequence 27, App1
20	42.5	53.8	37	1	US-08-477-383-27	Sequence 27, App1
21	42.5	53.8	37	1	US-08-477-383-27	Sequence 27, App1
22	42.5	53.8	37	1	US-08-487-174-27	Sequence 27, App1
23	42.5	53.8	37	1	US-08-480-750-27	Sequence 27, App1
24	42.5	53.8	38	1	US-08-137-800-25	Sequence 25, App1
25	42.5	53.8	38	1	US-08-477-383-25	Sequence 25, App1
26	42.5	53.8	38	1	US-08-487-174-25	Sequence 25, App1
27	42.5	53.8	38	1	US-08-480-750-25	Sequence 25, App1

## ALIGNMENTS

RESULT 1  
 US-09-336-536-65

; Sequence 65, Application US/09336536

; GENERAL INFORMATION:

; Patent No. 6406894

; APPLICANT: Leiby, K.

; APPLICANT: McKay, C.

; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF

; FILE REFERENCE: 7853-144

; CURRENT APPLICATION NUMBER: US/09/336, 536

; CURRENT FILING DATE: 1999-06-18

; NUMBER OF SEQ ID NOS: 75

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 65

; LENGTH: 56

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-336-536-65

Query Match 57.0%; Score 45; DB 4; Length 56;

Best Local Similarity 63.6%; Pred. No. 7.6%; Mismatches 3; Indels 0; Gaps 0;

RESULT 2  
 US-09-336-536-60

; Sequence 60, Application US/09336536

; GENERAL INFORMATION:

; Patent No. 6406894

; APPLICANT: Leiby, K.

; APPLICANT: McKay, C.

; TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF

; FILE REFERENCE: 7853-144

; CURRENT APPLICATION NUMBER: US/09/336, 536

; CURRENT FILING DATE: 1999-06-18

; NUMBER OF SEQ ID NOS: 75

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO: 60

; LENGTH: 187

; TYPE: PRT

; ORGANISM: Mus musculus

US-09-336-536-60

Query Match 57.0%; Score 45; DB 4; Length 187;

RESULT 3  
 US-09-336-536-58  
 / Sequence 58, Application US/09336536  
 / GENERAL INFORMATION:  
 / APPLICANT: Bossons, S.  
 / APPLICANT: Leiby, K.  
 / TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF  
 / FILE REFERENCE: 7853-144  
 / CURRENT APPLICATION NUMBER: US/09/336,536  
 / CURRENT FILING DATE: 1999-06-18  
 / NUMBER OF SEQ ID NOS: 75  
 / SOFTWARE: PatentIn Ver. 2.0  
 / SEQ ID NO: 58  
 / LENGTH: 213  
 / TYPE: PRT  
 / ORGANISM: Mus musculus  
 / US-09-336-536-58

Query Match 57.0%; Score 45; DB 4; Length 213;  
 Best Local Similarity 63.6%; Pred. No. 24;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 SVCCGYKLCFP 11  
 Db 132 SCCCLYKXCCP 142

RESULT 4  
 US-09-914-259-13  
 / Sequence 13, Application US/09914259  
 / GENERAL INFORMATION:  
 / APPLICANT: Makowski, Lee  
 / APPLICANT: Hyman, Paul  
 / APPLICANT: Williams, Mark  
 / TITLE OF INVENTION: STAGED ASSEMBLY OF NANOSTRUCTURES  
 / FILE REFERENCE: 8471-01-999  
 / CURRENT APPLICATION NUMBER: US/09/914,259  
 / CURRENT FILING DATE: 2000-11-21  
 / NUMBER OF SEQ ID NOS: 180  
 / SOFTWARE: FastSEQ for Windows version 4.0  
 / LENGTH: 503  
 / TYPE: PRT  
 / ORGANISM: Drosophila melanogaster  
 / US-09-914-259-13

Query Match 55.7%; Score 44; DB 4; Length 503;  
 Best Local Similarity 55.6%; Pred. No. 71;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CGYKLCFPC 12  
 Db 150 CGHRFMNP 158

RESULT 5  
 US-08-137-800-29  
 / Sequence 29, Application US/08137800  
 / GENERAL INFORMATION:  
 / APPLICANT: Olivera, Baldomero M.  
 / APPLICANT: Cruz, Lourdes J.  
 / APPLICANT: Hillyard, David R.  
 / APPLICANT: Macintosh, J. Michael  
 / APPLICANT: Santos, Amerifino S.  
 / TITLE OF INVENTION: Conotoxin Peptides  
 / NUMBER OF SEQUENCES: 59  
 / CORRESPONDENCE ADDRESS: Venable, Baetjer, Howard & Civiletti  
 / STREET: 1201 New York Avenue, N.W., Suite 1000  
 / CITY: Washington  
 / STATE: DC  
 / COUNTRY: U.S.A.  
 / ZLP: 20005  
 / COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/477, 383  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/137, 800  
 FILING DATE: 19-OCT-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/084, 848  
 FILING DATE: 29-JUN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ihnen, Jeffrey L.  
 REGISTRATION NUMBER: 28, 957  
 REFERENCE/DOCKET NUMBER: 24260-107673  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-962-4810  
 TELEFAX: 202-962-8300  
 INFORMATION FOR SEQ ID NO: 29:  
 LENGTH: 38 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ORIGINAL SOURCE:  
 LENGTH: 38 amino acids  
 TYPE: amino acid  
 ORGANISM: Conus stercusmuscarum  
 FEATURE:  
 NAME/KEY: Modified-site  
 LOCATION: 38  
 OTHER INFORMATION: /note= "Xaa is des-Xaa or Gly-Arg-Arg-Asn-His. When Xaa is des-Xaa the C-terminus is preferably amidated."  
 US-08-477-383-29

RESULT 7  
 Query Match Score 43.5; DB 1; Length 38;  
 Best Local Similarity 46.7%; Pred. No. 8.7%;  
 Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;  
 Db 10 TTCCGYDPGSMCPPC 24

RESULT 8  
 US-08-480-750-29  
 Sequence 29, Application US/08480750  
 Patent No. 5633347  
 GENERAL INFORMATION:  
 APPLICANT: Olivera, Baldomero M.  
 APPLICANT: Cruz, Lourdes J.  
 APPLICANT: Hilliard, David R.  
 APPLICANT: MacIntosh, J. Michael  
 APPLICANT: Santos, Ameurfino S.  
 TITLE OF INVENTION: Conotoxin Peptides  
 NUMBER OF SEQUENCES: 59  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
 STREET: 1201 New York Avenue, N.W., Suite 1000  
 CITY: Washington  
 STATE: DC  
 COUNTRY: U.S.A.  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/480,750  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/137, 800

FILING DATE: 19-OCT-1993  
 PRIORITY NUMBER: US 08/084,848  
 FILING DATE: 29-JUN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ihnen, Jeffrey L.  
 REGISTRATION NUMBER: 28,957  
 REFEERENCE/DOCKET NUMBER: 24260-107673  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-962-4810  
 TELEFAX: 202-962-8300  
 INFORMATION FOR SEQ ID NO: 59:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 38 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 HYPOTHETICAL: NO  
 ORIGINAL SOURCE: Conus stercusmuscarum  
 ORGANISM: Conus stercusmuscarum  
 FEATURES:  
 NAME/KEY: Modified-site  
 LOCATION: 38  
 OTHER INFORMATION: "note= "Xaa is des-Xaa or  
 OTHER INFORMATION: Gly-Arg-Arg-Asn-His. When Xaa is des-Xaa the C-terminus is  
 OTHER INFORMATION: preferably amidated."  
 US-08-480-750-29

Query Match Score 43.5%; DB 1; Length 38;  
 Best Local Similarity 46.7%; Pred. No. 8.7;  
 Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

Qy 1 SVCCGY--KLCFPC 12  
 Db : ||||| : | |  
 10 TICCGYDPGSMCPC 24

RESULT 9  
 US-08-477-383-59  
 Sequence 59, Application US/08477383  
 Patent No. 5599340  
 GENERAL INFORMATION:  
 APPLICANT: Olivera, Baldomero M.  
 APPLICANT: Cruz, Lourdes J.  
 APPLICANT: Macintosh, David R.  
 APPLICANT: Santos, Ameurino S.  
 TITLE OF INVENTION: Conotoxin Peptides  
 NUMBER OF SEQUENCES: 59  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Venable, Baetjer, Howard & Civiletti  
 STREET: 1201 New York Avenue, N.W., Suite 1000  
 CITY: Washington  
 STATE: DC  
 COUNTRY: U.S.A.  
 ZIP: 20005

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 FILING DATE: 19-OCT-1993  
 PRIORITY NUMBER: US 08/137,800  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/137,800  
 FILING DATE: 19-OCT-1993  
 PRIORITY NUMBER: US 08/084,848  
 FILING DATE: 29-JUN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ihnen, Jeffrey L.  
 REGISTRATION NUMBER: 28,957  
 REFEERENCE/DOCKET NUMBER: 24260-107673  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-962-4810  
 INFORMATION FOR SEQ ID NO: 59:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 42 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:

TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ORIGINAL SOURCE:  
 ORGANISM: *Conus stercusmuscarum*  
 US-08-487-174-59

Query Match 55.1%; Score 43.5%; DB 1; Length 42;  
 Best Local Similarity 46.7%; Pred. No. 9.4%;  
 Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

Qy 1 SVCCGY---KLCFPC 12  
 Db 10 TTCCGYDPGSMCPPC 24

RESULT 11  
 US-08-480-750-59  
 ; Sequence 59, Application US/08480750  
 ; Patent No. 5633347  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Olvera, Baldomero M.  
 ; APPLICANT: Cruz, Lourdes J.  
 ; APPLICANT: Hillyard, David R.  
 ; APPLICANT: Macintosh, J. Michael  
 ; APPLICANT: Santos, Ameurfina S.  
 ; TITLE OF INVENTION: Conotoxin Peptides  
 ; NUMBER OF SEQUENCES: 53  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
 ; STREET: 1201 New York Avenue N.W., Suite 1000  
 ; CITY: Washington  
 ; STATE: DC  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: WordPerfect 5.1  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/137,800  
 ; FILING DATE: 19-OCT-1993  
 ; CLASSIFICATION: 530  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Innen, Jeffrey L.  
 ; REGISTRATION NUMBER: 28,957  
 ; REFERENCE/DOCKET NUMBER: 24260-104763  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-962-4810  
 ; TELEFAX: 202-962-8300  
 ; INFORMATION FOR SEQ ID NO: 44:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 80 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; HYPOTHETICAL: NO  
 ; ANTI-SENSE: NO  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: *Conus stercusmuscarum*  
 ; US-08-137-800-44

Query Match 55.1%; Score 43.5%; DB 1; Length 80;  
 Best Local Similarity 46.7%; Pred. No. 17; Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

Qy 1 SVCCGY---KLCFPC 12  
 Db 48 TTCCGYDPGSMCPPC 62

RESULT 13  
 US-08-477-383-44  
 ; Sequence 44, Application US/08477383  
 ; Patent No. 5589340  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Olvera, Baldomero M.  
 ; APPLICANT: Cruz, Lourdes J.  
 ; APPLICANT: Hillyard, David R.  
 ; APPLICANT: Macintosh, J. Michael  
 ; APPLICANT: Santos, Ameurfina S.  
 ; TITLE OF INVENTION: Conotoxin Peptides  
 ; NUMBER OF SEQUENCES: 59  
 ; CORRESPONDENCE ADDRESS:

Query Match 55.1%; Score 43.5%; DB 1; Length 42;  
 Best Local Similarity 46.7%; Pred. No. 9.4%; Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

ADDRESSEE: Venable, Baetjer, Howard & Civiletti  
 STREET: 1201 New York Avenue, N.W., Suite 1000  
 CITY: Washington  
 STATE: DC  
 COUNTRY: U.S.A.  
 ZIP: 20005

COMPUTER READABLE FORM:  
 COMPUTER: IBM PC compatible  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/477,383  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/137,800  
 FILING DATE: 19-OCT-1993

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/084,848  
 FILING DATE: 29-JUN-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Ihnen, Jeffrey L.  
 REGISTRATION NUMBER: 28,957  
 REFERENCE DOCKET NUMBER: 24260-107673  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-962-4810  
 TELEFAX: 202-962-8300

SEQUENCE CHARACTERISTICS:  
 LENGTH: 80 amino acids  
 TYPE: amino acid  
 STRANDEDNESS:  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 HYPOTHETICAL: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Conus stercusmuscarum  
 US-08-477-383-44

RESULT 14  
 US-08-487-174-44  
 Sequence 4, Application US/08487174  
 Patent No. 5595972  
 GENERAL INFORMATION:  
 APPLICANT: Cruz, Lourdes J.R.  
 APPLICANT: Macintoch, J. Michael  
 APPLICANT: Santos, Amerifino S.  
 TITLE OF INVENTION: Conotoxin Peptides  
 NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:  
 ADDRESS: Venable, Baetjer, Howard & Civiletti  
 STREET: 1201 New York Avenue, N.W., Suite 1000  
 CITY: Washington  
 STATE: DC  
 ZIP: 20005

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/480,750  
 FILING DATE: 07-JUN-1995  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/08/137,800  
 FILING DATE: 19-OCT-1993  
 ATTORNEY/AGENT INFORMATION:

; NAME: Innen, Jeffrey L.  
; REGISTRATION NUMBER: 28,957  
; TELECOMMUNICATION INFORMATION:  
; REFERENCE/DOCKET NUMBER: 24260-107673  
; TELEPHONE: 202-962-4810  
; TELEFAX: 202-962-8300  
; INFORMATION FOR SEQ ID NO: 44:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 80  
; STRANDEDNESS:  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Conus stercusmuscarum  
; US-08-480-750-44

Query Match 55.1%; Score 43.5; DB 1; Length 80;  
Best Local Similarity 46.7%; Pred. No. 17;  
Matches 7; Conservative 2; Mismatches 3; Indels 3; Gaps 1;  
STRINGS: SVCCGY--KLCFPC 12  
Db 48 TRCCCGYDPGSMCPPC 62

Search completed: August 10, 2004, 16:05:36  
Job time : 4.7027 secs

John Scott

GenCore version 5.1.6  
(c) 1993 - 2004 Compugen Ltd.

Copyright (c) 1993 - 2004 Compugen Ltd.

OM Protein - protein search, using SW model

Run on: August 10, 2004, 16:04:26 ; Search time 13.1351 Seconds  
(without alignments)  
286.575 Million cell updates/sec

Title: US-10-072-602B-534

Perfect score: 79

Sequence: 1 SVCCGYKLCFPC 12

Scoring table: BLOSUM62

Gapext 10.0 , Gapext 0.5

Searched: 1291235 seqs, 31362936 residues

Total number of hits satisfying chosen parameters: 1291235

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing First 45 summaries

Database : Published Applications AA:<sup>\*</sup>

```

1: /cgn2_6/podata/2/pubpaas/US07_PUBCOMB.pep:*
2: /cgn2_6/podata/2/pubpaas/PCT_US06_NEW_PUB.pep:*
3: /cgn2_6/podata/2/pubpaas/US06_NEW_PUB.pep:*
4: /cgn2_6/podata/2/pubpaas/US05_PUBCOMB.pep:*
5: /cgn2_6/podata/2/pubpaas/US07_NEW_PUB.pep:*
6: /cgn2_6/podata/2/pubpaas/PCUTS_PUBCOMB.pep:*
7: /cgn2_6/podata/2/pubpaas/US08_NEW_PUB.pep:*
8: /cgn2_6/podata/2/pubpaas/US08_PUBCOMB.pep:*
9: /cgn2_6/podata/2/pubpaas/US09_PUBCOMB.pep:*
10: /cgn2_6/podata/2/pubpaas/US09B_PUBCOMB.pep:*
11: /cgn2_6/podata/2/pubpaas/US09C_PUBCOMB.pep:*
12: /cgn2_6/podata/2/pubpaas/US09_NEW_PUB.pep:*
13: /cgn2_6/podata/2/pubpaas/US1A_PUBCOMB.pep:*
14: /cgn2_6/podata/2/pubpaas/US1A_PUBCOMB.pep:*
15: /cgn2_6/podata/2/pubpaas/US1C_PUBCOMB.pep:*
16: /cgn2_6/podata/2/pubpaas/US10_NEW_PUB.pep:*
17: /cgn2_6/podata/2/pubpaas/US60_NEW_PUB.pep:*
18: /cgn2_6/podata/2/pubpaas/US60_PUBCOMB.pep:*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query Match	Length	DB ID	Description
1	79	100.0	12	14	US-10-072-602B-534
2	69	100.0	62	14	US-10-072-602B-534
3	69	87.3	13	14	US-10-072-602B-534
4	69	87.3	61	14	US-10-072-602B-534
5	68	86.1	61	14	US-10-072-602B-545
6	63	79.7	11	14	US-10-072-602B-524
7	63	79.7	11	14	US-10-072-602B-533
8	63	79.7	12	14	US-10-072-602B-527
9	63	79.7	12	14	US-10-072-602B-528
10	63	79.7	13	14	US-10-072-602B-525
11	63	79.7	13	14	US-10-072-602B-526
12	63	79.7	13	14	US-10-072-602B-535
13	63	79.7	13	14	US-10-072-602B-538
14	63	79.7	16	14	US-10-072-602B-355
15	63	79.7	61	14	US-10-072-602B-62

Sequence 349, APP  
Sequence 339, APP  
Sequence 162, APP  
Sequence 333, APP  
Sequence 342, APP  
Sequence 364, APP  
Sequence 353, APP  
Sequence 523, APP  
Sequence 532, APP  
Sequence 536, APP  
Sequence 531, APP  
Sequence 229, APP  
Sequence 358, APP  
Sequence 537, APP  
Sequence 361, APP  
Sequence 539, APP  
Sequence 367, APP  
Sequence 340, APP  
Sequence 163, APP  
Sequence 334, APP  
Sequence 365, APP  
Sequence 530, APP  
Sequence 331, APP  
Sequence 336, APP  
Sequence 34, APP1  
Sequence 163, APP  
Sequence 346, APP  
Sequence 161903, APP  
Sequence 5609, APP  
Sequence 362, APP

**ALIGNMENTS**

RESULT 1  
US-10-072-602B-534 ; Application US-10072602B  
; Publication No. US20030109670A1  
; GENERAL INFORMATION:  
; APPLICATION: Cognex, Inc.  
; ATTORNEY: Oliver, Baldomero M.  
; ATTORNEY: McIntosh, J., Michael L.  
; ATTORNEY: Watkins, Maren  
; ATTORNEY: Garrett, James E.  
; ATTORNEY: Cruz, Lourdes J.  
; ATTORNEY: Grilley, Michelle  
; ATTORNEY: Schoenfeld, Robert M.  
; ATTORNEY: Walker, Craig  
; ATTORNEY: Shetty, Reshma  
; ATTORNEY: Jones, Robert M.  
; TITLE OF INVENTION: Cone Snail Peptides  
; FILE REFERENCE: 2314-249  
; CURRENT APPLICATION NUMBER: US-10-072-602B  
; CURRENT FILING DATE: 2002-02-11  
; PRIOR APPLICATION NUMBER: US-10-267-408  
; PRIOR FILING DATE: 2001-02-09  
; NUMBER OF SEQ ID NOS: 638  
; SOFTWARE: Patentin version 3.0  
; SEQ ID NO 534  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Conus aulicus  
; SEQ ID NO 534  
; Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 12; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;

QY 1 SVCCGYKLCFPC 12  
Db 1 SVCCGYKLCFPC 12

RESULT 2  
 US-10-072-602B-352  
 ; Sequence 352, Application US/10072602B  
 ; Publication No. US20030109670A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Utah Research Foundation  
 ; APPLICANT: Cognetix, Inc.  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: McIntosh, J., Michael  
 ; APPLICANT: Watkins, Maren  
 ; APPLICANT: Garrett, James E.  
 ; APPLICANT: Cruz, Lourdes J.  
 ; APPLICANT: Grillee, Michelle  
 ; APPLICANT: Schoenfeld, Robert M.  
 ; APPLICANT: Walker, Craig  
 ; APPLICANT: Shetty, Reshma  
 ; APPLICANT: Jones, Robert M.  
 ; TITLE OF INVENTION: Cone Snail Peptides  
 ; FILE REFERENCE: 2314-249  
 ; CURRENT APPLICATION NUMBER: US/10/072,602B  
 ; CURRENT FILING DATE: 2002-02-11  
 ; PRIOR APPLICATION NUMBER: US 60/267,408  
 ; PRIOR FILING DATE: 2001-02-09  
 ; NUMBER OF SEQ ID NOS: 638  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 352  
 ; LENGTH: 62  
 ; TYPE: PRT  
 ; ORGANISM: Conus aulicus  
 US-10-072-602B-352

Query Match 100.0%; Score 79; DB 14; Length 62;  
 Best Local Similarity 100%; Pred. No. 0.0012; Indels 0;  
 Matches 12; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 SVCCGYKLCPFC 12  
 Db 50 SVCCGYKLCPFC 61

RESULT 3  
 US-10-072-602B-529  
 ; Sequence 529, Application US/10072602B  
 ; Publication No. US20030109670A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Utah Research Foundation  
 ; APPLICANT: Cognetix, Inc.  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: McIntosh, J., Michael  
 ; APPLICANT: Watkins, Maren  
 ; APPLICANT: Garrett, James E.  
 ; APPLICANT: Cruz, Lourdes J.  
 ; APPLICANT: Grillee, Michelle  
 ; APPLICANT: Schoenfeld, Robert M.  
 ; APPLICANT: Walker, Craig  
 ; APPLICANT: Shetty, Reshma  
 ; APPLICANT: Jones, Robert M.  
 ; TITLE OF INVENTION: Cone Snail Peptides  
 ; FILE REFERENCE: 2314-249  
 ; CURRENT APPLICATION NUMBER: US/10/072,602B  
 ; CURRENT FILING DATE: 2002-02-11  
 ; PRIOR APPLICATION NUMBER: US 60/267,408  
 ; PRIOR FILING DATE: 2001-02-09  
 ; NUMBER OF SEQ ID NOS: 638  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 529  
 ; LENGTH: 13  
 ; TYPE: PRT  
 ; ORGANISM: Conus marmoreus  
 US-10-072-602B-529

Query Match 87.3%; Score 69; DB 14; Length 13;  
 Best Local Similarity 90.9%; Pred. No. 0.007; Indels 1;  
 Matches 10; Conservative 0; Mismatches 1; Gaps 0;

Qy 2 VCCGYKLCPFC 12  
 Db 3 VCCGYKLCPFC 13

RESULT 4  
 US-10-072-602B-330  
 ; Sequence 330, Application US/10072602B  
 ; Publication No. US20030109670A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Utah Research Foundation  
 ; APPLICANT: Cognetix, Inc.  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: McIntosh, J., Michael  
 ; APPLICANT: Watkins, Maren  
 ; APPLICANT: Garrett, James E.  
 ; APPLICANT: Cruz, Lourdes J.  
 ; APPLICANT: Grillee, Michelle  
 ; APPLICANT: Schoenfeld, Robert M.  
 ; APPLICANT: Walker, Craig  
 ; APPLICANT: Shetty, Reshma  
 ; APPLICANT: Jones, Robert M.  
 ; TITLE OF INVENTION: Cone Snail Peptides  
 ; FILE REFERENCE: 2314-249  
 ; CURRENT APPLICATION NUMBER: US/10/072,602B  
 ; CURRENT FILING DATE: 2002-02-11  
 ; PRIOR APPLICATION NUMBER: US 60/267,408  
 ; PRIOR FILING DATE: 2001-02-09  
 ; NUMBER OF SEQ ID NOS: 638  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 330  
 ; TYPE: PRT  
 ; ORGANISM: Conus marmoreus  
 US-10-072-602B-330

Query Match 87.3%; Score 69; DB 14; Length 61;  
 Best Local Similarity 90.9%; Pred. No. 0.026; Indels 1;  
 Matches 10; Conservative 0; Mismatches 1; Gaps 0;

Qy 2 VCCGYKLCPFC 12  
 Db 51 VCCGYKLCPFC 61

RESULT 5  
 US-10-072-602B-345  
 ; Sequence 345, Application US/10072602B  
 ; Publication No. US20030109670A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: University of Utah Research Foundation  
 ; APPLICANT: Cognetix, Inc.  
 ; APPLICANT: Olivera, Baldomero M.  
 ; APPLICANT: McIntosh, J., Michael  
 ; APPLICANT: Watkins, Maren  
 ; APPLICANT: Garrett, James E.  
 ; APPLICANT: Cruz, Lourdes J.  
 ; APPLICANT: Grillee, Michelle  
 ; APPLICANT: Schoenfeld, Robert M.  
 ; APPLICANT: Walker, Craig  
 ; APPLICANT: Shetty, Reshma  
 ; APPLICANT: Jones, Robert M.  
 ; TITLE OF INVENTION: Cone Snail Peptides  
 ; FILE REFERENCE: 2314-249  
 ; CURRENT APPLICATION NUMBER: US/10/072,602B  
 ; CURRENT FILING DATE: 2002-02-11  
 ; PRIOR APPLICATION NUMBER: US 60/267,408  
 ; PRIOR FILING DATE: 2001-02-09  
 ; NUMBER OF SEQ ID NOS: 638  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO: 345  
 ; LENGTH: 61  
 ; TYPE: PRT  
 ; ORGANISM: Conus marmoreus  
 US-10-072-602B-345

```

; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 345
; LENGTH: 61
; TYPE: PRT
; ORGANISM: Conus marmoreus
US-10-072-602B-345

Query Match 86.1%; Score 68; DB 14; Length 61;
Best Local Similarity 90.9%; Pred. No. 0.036; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
; SEQ ID NO: 533
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Conus bandanus
US-10-072-602B-533

Query Match 79.7%; Score 63; DB 14; Length 11;
Best Local Similarity 90.8%; Pred. No. 0.039; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 CCGYKLCPPC 12
Db 2 CCGYKLCSPC 11

RESULT 8
US-10-072-602B-527
; Sequence 527, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Baldomero M. McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grillely, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072-602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SEQ ID NO: 524
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Conus bandanus
US-10-072-602B-524

Query Match 79.7%; Score 63; DB 14; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.039; Indels 0; Gaps 0;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 3 CCGYKLCPPC 12
Db 2 CCGYKLCSPC 11

RESULT 7
US-10-072-602B-533
; Sequence 533, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Baldomero M. McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grillely, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072-602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SEQ ID NO: 527
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Conus pennaceus
US-10-072-602B-527

Query Match 79.7%; Score 63; DB 14; Length 12;
Best Local Similarity 66.7%; Pred. No. 0.042; Indels 0; Gaps 0;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 SVCCGYKLCPPC 12
Db 1 STCCGFRMCIPC 12

RESULT 9
US-10-072-602B-528
; Sequence 528, Application US/10072602B
; Publication No. US20030109670A1
; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Baldomero M. McIntosh, J. Michael
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grillely, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 2314-249
; CURRENT APPLICATION NUMBER: US/10/072-602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SEQ ID NO: 528
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Conus pennaceus
US-10-072-602B-528

```

```

; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle M.
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; FILE REFERENCE: 23:14-249
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 528
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Conus episcopatus
US-10-072-602B-528

Query Match 79.7%; Score 63; DB 14; Length 12;
Best Local Similarity 66.7%; Pred. No. 0.042;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
TYPE: PRT
Qy 1 SVCCGYKLCFPC 12
Db 1 STCCGFRMCIPC 12

RESULT 10
US-10-072-602B-525
; Sequence 525, Application US/10072602B

; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J., Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 525
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Conus pennaceus
US-10-072-602B-525

Query Match 79.7%; Score 63; DB 14; Length 13;
Best Local Similarity 66.7%; Pred. No. 0.045;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
TYPE: PRT
Qy 1 SVCCGYKLCFPC 12
Db 1 STCCGFRMCIPC 12

RESULT 11
US-10-072-602B-526
; Sequence 526, Application US/10072602B

; GENERAL INFORMATION:
; APPLICANT: University of Utah Research Foundation
; APPLICANT: Cognetix, Inc.
; APPLICANT: Olivera, Baldomero M.
; APPLICANT: McIntosh, J., Michael
; APPLICANT: Watkins, Maren
; APPLICANT: Garrett, James E.
; APPLICANT: Cruz, Lourdes J.
; APPLICANT: Grilley, Michelle
; APPLICANT: Schoenfeld, Robert M.
; APPLICANT: Walker, Craig
; APPLICANT: Shetty, Reshma
; APPLICANT: Jones, Robert M.
; TITLE OF INVENTION: Cone Snail Peptides
; CURRENT APPLICATION NUMBER: US/10/072,602B
; CURRENT FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/267,408
; PRIOR FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 535
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Conus textile
US-10-072-602B-526

Query Match 79.7%; Score 63; DB 14; Length 13;
Best Local Similarity 72.7%; Pred. No. 0.045;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
TYPE: PRT
Qy 2 VCCGYKLCFPC 12
Db

```

Db 3 |||||::| vCCGYRMCVPC 13

RESULT 13 US-10-072-602B-538 ; Sequence 538, Application US/1072602B

; Publication No. US20030109670A1

; GENERAL INFORMATION:

; APPLICANT: University of Utah Research Foundation

; APPLICANT: Cognetix, Inc.

; APPLICANT: Olivera, Baldomero M.

; APPLICANT: McIntosh, J., Michael J.

; APPLICANT: Watkins, Maren

; APPLICANT: Garrett, James E.

; APPLICANT: Cruz, Lourdes J.

; APPLICANT: Grilley, Michelle

; APPLICANT: Schoenfeld, Robert M.

; APPLICANT: Walker, Craig

; APPLICANT: Shetty, Reshma

; APPLICANT: Jones, Robert M.

TITLE OF INVENTION: Cone Snail Peptides

FILE REFERENCE: 2314-249

CURRENT APPLICATION NUMBER: US/10/072-602B

CURRENT FILING DATE: 2002-02-11

PRIOR APPLICATION NUMBER: US 60/267,408

PRIOR FILING DATE: 2001-02-09

NUMBER OF SEQ ID NOS: 638

SEQUENCE: PatentIn version 3.0

SEQ ID NO: 538

LENGTH: 13

TYPE: PRT

ORGANISM: Conus pennaceus

US-10-072-602B-538

Query Match 79.7%; Score 63; DB 14; Length 13;

Best Local Similarity 66.7%; Pred. No. 0.045;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Db 1 SVCCGYRUCFPC 12

1 STCCGFRMCVPC 12

RESULT 14 US-10-072-602B-355 ; Sequence 355, Application US/1072602B

; Publication No. US20030109670A1

; GENERAL INFORMATION:

; APPLICANT: University of Utah Research Foundation

; APPLICANT: Cognetix, Inc.

; APPLICANT: Olivera, Baldomero M.

; APPLICANT: McIntosh, J., Michael J.

; APPLICANT: Watkins, Maren

; APPLICANT: Garrett, James E.

; APPLICANT: Cruz, Lourdes J.

; APPLICANT: Grilley, Michelle

; APPLICANT: Schoenfeld, Robert M.

TITLE OF INVENTION: Cone Snail Peptides

FILE REFERENCE: 2314-249

CURRENT APPLICATION NUMBER: US/10/072-602B

CURRENT FILING DATE: 2002-02-11

PRIOR APPLICATION NUMBER: US 60/267,408

PRIOR FILING DATE: 2001-02-09

NUMBER OF SEQ ID NOS: 638

SEQUENCE: PatentIn version 3.0

SEQ ID NO: 355

LENGTH: 16

TYPE: PPT

ORGANISM: Conus textile

US-10-072-602B-355

Query Match 79.7%; Score 63; DB 14; Length 16;

Best Local Similarity 72.7%; Pred. No. 0.053;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VCCGYKUCFPC 12

5 vCCGYRMCVPC 15

Db 5 vCCGYRMCVPC 15

RESULT 15 US-10-072-602B-62 ; Sequence 62, Application US/10072602B

; Publication No. US20030109670A1

; GENERAL INFORMATION:

; APPLICANT: University of Utah Research Foundation

; APPLICANT: Cognetix, Inc.

; APPLICANT: Olivera, Baldomero M.

; APPLICANT: McIntosh, J., Michael J.

; APPLICANT: Watkins, Maren

; APPLICANT: Garrett, James E.

; APPLICANT: Cruz, Lourdes J.

; APPLICANT: Grilley, Michelle

; APPLICANT: Schoenfeld, Robert M.

; APPLICANT: Walker, Craig

; APPLICANT: Shetty, Reshma

; APPLICANT: Jones, Robert M.

TITLE OF INVENTION: Cone Snail Peptides

FILE REFERENCE: 2314-249

CURRENT APPLICATION NUMBER: US/10/072-602B

PRIOR APPLICATION NUMBER: 2002-02-11

PRIOR FILING DATE: 2001-02-09

NUMBER OF SEQ ID NOS: 638

SEQUENCE: PatentIn version 3.0

SEQ ID NO: 62

LENGTH: 61

TYPE: PPT

ORGANISM: Conus bandanus

US-10-072-602B-62

Query Match 79.7%; Score 63; DB 14; Length 61;

Best Local Similarity 90.0%; Pred. No. 0.17;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCGYKLCFPC 12

52 CCGYKLCSPC 61

Db 52 CCGYKLCSPC 61

Search completed: August 10, 2004, 16:13:54

Job time : 13.1351 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: August 10, 2004, 16:00:00 ; Search time 3.72973 Seconds  
 Perfect score: 79  
 Sequence: 1 SVCCGYKLCFPC 12

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5  
 Searched:

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

## Listing First 45 summaries

Database : PIR 78:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

## RESULT 1

T30368

probable immediate-early transactivator

0 - Lymantria dispar nuclear polyhedrosis virus

C;Species: Lymantria dispar nuclear polyhedrosis virus, LdMPV

C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999

C;Accession: T30368

R;Kuzio, J.; Pearson, M.N.; Harwood, S.H.; Funk, C.J.; Evans, J.T.; Slavicek, J.M.; Rohr

Virology 253, 17-34, 1999

A;Title: Sequence and analysis of the genome of a baculovirus pathogenic for Lymantria d

A;Reference number: 220834; MUID:99124785; PMID:9887315

A;Status: Preliminary; translated from GB/EMBL/DDJB

A;Accession: T30368

A;Residues: 1-258 &lt;KUZ&gt;

A;Cross-references: EMBL:AF081810; PIDN: AAC70206.1

C;Keywords: immediate-early protein

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	67.1	258	2 T30368	Probable immediate testis specific protein
2	50	63.3	55	2 S25774	hypothetical prote
3	50	63.3	514	2 T10559	hypothetical prote
4	49	62.0	428	2 T46025	immediate early pr
5	47	59.5	245	2 T10407	hypothetical prote
6	47	59.5	373	2 T47488	hypothetical prote
7	47	59.5	470	2 CB8256	hypothetical prote
8	47	59.5	525	2 T10574	hypothetical prote
9	44	55.7	342	1 F64141	probable L-iditol
10	44	55.7	361	2 T15243	hypothetical prote
11	43	54.4	78	2 T50943	probable ferredoxi
12	43	54.4	186	2 A45310	ultra-high-sulfur
13	43	54.4	222	2 T47487	hypothetical prote
14	43	54.4	373	2 EB4647	hypothetical prote
15	43	54.4	484	2 T20554	hypothetical prote
16	43	54.4	659	2 T01520	hypothetical prote
17	42	53.2	350	2 G84647	probable transcript
18	42	53.2	434	2 A4352	hypothetical prote
19	42	53.2	512	2 F86193	probable CHP-rich
20	42	53.2	658	2 F85024	hypothetical prote
21	42	53.2	715	2 S77439	protein FN21.2 [i
22	41	51.9	69	2 A96696	probable RING zinc
23	41	51.9	137	2 G96779	hypothetical prote
24	41	51.9	193	2 T09443	protein F18014.3 [
25	41	51.9	226	2 E86326	probable RING zinc
26	41	51.9	227	2 T02413	hypothetical prote
27	41	51.9	235	2 T1928	RING finger prote
28	41	51.9	249	2 T52142	RING zinc finger p
29	41	51.9	264	2 T08939	

## ALIGNMENTS

homeodomain trans	30	41	51.9	332	2 HB4443
hypothetical prote	31	41	51.9	348	2 T47494
hypothetical prote	32	41	51.9	402	2 T52522
hypothetical prote	33	41	51.9	404	2 T02396
hypothetical prote	34	41	51.9	890	2 T21000
hypothetical prote	35	41	51.9	1885	2 JQ2183
hypothetical prote	36	40.5	51.3	436	2 HB7793
protein C2TA12.8 [	37	40.5	51.3	497	2 GB7793
hypothetical prote	38	40	50.6	180	2 T09063
granulocyte colony	39	40	50.6	207	2 A4573
similar to Ariadne	40	40	50.6	542	2 AB4725
lymphocyte antigen	41	40	50.6	567	2 S29498
zK652.5 protein -	42	40	50.6	580	2 S44908
hypothetical prote	43	40	50.6	719	2 T47727
erythrocyte membra	44	40	50.6	1729	2 T18396
chloride channel P	45	39.5	50.0	764	2 T07608

A;Reference number: Z17011; MUID:97271300; PMID:9126251  
A;Accession: T10407  
A;Status: preliminary; translated from GB/EMBL/DDBU  
A;Molecule type: DNA  
A;Residues: 1-245 <AHR>  
A;Cross-references: EMBL:U75930; NID:92934903; PID:g1911384

Query Match 59.5%; Score 47; DB 2; Length 245;  
Best Local Similarity 60.0%; Pred. No. 11;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CCGYKLCFPC 12  
Db 213 CCQYSLCYAC 222

RESULT 6

T41488 hypothetical protein F9K21.60 - *Arabidopsis thaliana*  
C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C;Accession: T44488  
R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke, K.  
Submitted to the Protein Sequence Database, February 2000  
A;Reference number: Z16533  
A;Accession: T10559  
A;Molecule type: DNA  
A;Residues: 1-514 <BEV>  
A;Cross-references: EMBL:AL050399; GSPDB:GN00062; ATSP:F25E4.10  
A;Experimental source: cultivar Columbia; BAC clone F25E4  
C;Genetics:  
A;Gene: ATSP:F25E4.10  
A;Map position: 4  
A;Introns: 436/3; 457/3; 479/3  
Query Match 63.3%; Score 50; DB 2; Length 514;  
Best Local Similarity 70.0%; Pred. No. 7.3%;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CCGYKLCFPC 12  
Db 295 CCGYVLCFCC 304

RESULT 4

T4025 hypothetical protein T10K17.240 - *Arabidopsis thaliana*  
C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
C;Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 02-Sep-2000  
C;Accession: T46025  
R;Benes, V.; Wurmback, B.; Drzonk, H.; Ansorge, W.; Mewes, H.W.; Lemcke, K.; Mayer, K.F.  
Submitted to the Protein Sequence Database, January 2000  
A;Reference number: Z23019  
A;Accession: T46025  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-428 <BEN>  
A;Cross-references: EMBL:AL132977  
C;Genetics:  
A;Map position: 3  
A;Note: T10K17.240  
A;Residues: 1-428 <BEN>  
A;Experimental source: cultivar Columbia; BAC clone T10K17  
C;Superfamily: RING finger homology <RNN>  
Query Match 62.0%; Score 49; DB 2; Length 428;  
Best Local Similarity 60.0%; Pred. No. 8.8%;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CCGYKLCFPC 12  
Db 145 CCGHLYCNP 154

RESULT 5

T0407 immediate early protein 0 - *Orgyia pseudotsugata* nuclear polyhedrosis virus  
C;Species: *Orgyia pseudotsugata* nuclear polyhedrosis virus, OpMNPV  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 11-May-2000  
C;Accession: T10407  
R;Ahrens, C.A.; Russell, R.R.; Funk, C.J.; Evans, J.; Harwood, S.; Rohrmann, G.F.  
Virology 229, 381-399, 1997  
A;Title: The sequence of the *Orgyia pseudotsugata* multinucleocapsid nuclear polyhedrosis

A;Reference number: Z17011; MUID:97271300; PMID:9126251  
A;Accession: T10407  
A;Status: preliminary; translated from GB/EMBL/DDBU  
A;Molecule type: DNA  
A;Residues: 1-245 <AHR>  
A;Cross-references: EMBL:U75930; NID:92934903; PID:g1911384

Query Match 59.5%; Score 47; DB 2; Length 470;  
Best Local Similarity 77.8%; Pred. No. 18;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CCGYKLCFPC 12  
Db 213 CCQYSLCYAC 222

RESULT 7

C86256 hypothetical protein [imported] - *Arabidopsis thaliana*  
C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C;Accession: C86256  
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.R.; Creasy, T.H.; Dewar, K., Hansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marziali, A.; Rooney, T.; Rowley, D.; Sakano, H.; Salzberg, S.L.; Schwartz, J.R.; Shimm, P.; Southwick, A.M.; Sun, H.; Tallon, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
A;Reference number: A66141; MUID:21016719; PMID:11130712  
A;Accession: C86256

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-470 <STO>  
A;Cross-references: GB:AE005172; NID:910086520; PIDN:AAG12580.1; GSPDB:GN00141  
C;Genetics:  
A;Map position: 1

Query Match 59.5%; Score 47; DB 2; Length 470;  
Best Local Similarity 77.8%; Pred. No. 18;  
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CCGYKLCFPC 12  
Db 213 CCQYSLCYAC 222

C;Species: Homo sapiens (man)  
 C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 23-Jul-1999  
 C;Accession: T12543  
 R;Wambutt, R.; Heubner, D.; Newes, H.W.; Gassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, June 1999  
 A;Reference number: 217524  
 A;Accession: T12543

**RESULT 8**

T1074  
 hypothetical protein F25E4.160 - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 15-Oct-1999  
 C;Accession: T1074  
 R;Bayan, M.; Leonard, N.; Quail, M.; Harris, B.; Rajandream, M.A.; Barrell, B.G.; Bancroft, M.; Lennard, N.; Reference number: 216533  
 A;Accession: T1074  
 A;Molecule type: DNA  
 A;Residues: 1-557 <BEV>  
 A;Cross-references: EMBL:AL050399; GSPDB:GN00062; ATSP:F25E4.160  
 A;Experimental source: cultivar Columbia; BAC clone F25E4  
 C;Genetics:  
 A;Genes: ATSP:F25E4.160  
 A;Map position: 4

Query Match Score 59.5%; Score 47; DB 2; Length 525;  
 Best Local Similarity 77.8%; Pred. No. 19;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match Score 4 CGYKLCFPC 12  
 Best Local Similarity 75.0%; Pred. No. 39;  
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match Score 5 GYKLCPFC 12  
 Best Local Similarity 55.7%; Pred. No. 39;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Query Match Score 5 GYKLCPFC 12  
 Best Local Similarity 55.7%; Pred. No. 39;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

**RESULT 9**

F64141  
 probable L-iditol 2-dehydrogenase (EC 1.1.1.14) H10053 - Haemophilus influenzae (strain N;Alternate names: sorbitol dehydrogenase  
 C;Species: Haemophilus influenzae  
 C;Accession: F64141  
 R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.R.; Gocayne, J.D.; Scott, J.; Shirlow, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M. Scien  
 A;Authors: Ghannoum, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, J.A.; Reference number: A64000; PMID: 95350630; PMID: 7542800  
 A;Accession: F64141  
 A;Status: nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-342 <TIGR>  
 A;Cross-references: GB:U32690; GB:L42023; NID:9157991; PID: AAC21731.1; PID:g1573000; I

A;Description: catalyzes the oxidation by NAD+ of sorbitol to fructose  
 C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology  
 C;Keywords: metalloprotein; NAD; oxidoreductase; zinc  
 P;26-311/Domain: long-chain alcohol dehydrogenase homology <IADH>  
 P;168-197/Region: beta-alpha-beta NAD nucleotide-binding fold  
 P;41,63-149/Binding site: zinc, catalytic (Cys, His, Glu) #status predicted  
 P;94,97,100,108/Binding site: zinc, noncatalytic (Cys) #status predicted

Query Match Score 55.7%; Score 44; DB 1; Length 342;  
 Best Local Similarity 63.6%; Pred. No. 38;  
 Matches 7; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

Query Match Score 2 VCCGYKLCFPC 12  
 Best Local Similarity 54.4%; Pred. No. 34;  
 Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Query Match Score 2 VCCGQ--CYPC 100  
 Best Local Similarity 54.4%; Pred. No. 34;  
 Matches 2; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

**RESULT 10**

T12543  
 hypothetical protein DKFZp434M154.1 - human (fragment)

C;Species: Homo sapiens (man)  
 C;Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 23-Jul-1999  
 C;Accession: T12543  
 R;Wambutt, R.; Heubner, D.; Newes, H.W.; Gassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, June 1999  
 A;Reference number: 217524  
 A;Accession: T12543

**RESULT 11**

T50943  
 probable ferredoxin DirA [imported] - Pseudomonas abietaniphila  
 C;Species: Pseudomonas abietaniphila  
 C;Accession: T50943  
 R;Martin, V.J.; Mohn, W.W.  
 J;Bacteriol. 181, 2675-2682, 1999  
 A;Title: A novel aromatic-C-ring-hydroxylating dioxygenase from the diterpenoid-degrading  
 A;Reference number: 225281; PMID: 9235742; PMID: 12171773  
 A;Accession: T50943  
 A;Status: preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: DNA  
 A;Residues: 1-78 <MR>  
 A;Cross-references: EMBL:AF119621; PID:NAAD21062.1  
 A;Experimental source: strain BMKE-9; ATCC700689  
 C;Genetics:  
 A;Gene: dla3

Query Match Score 54.4%; Score 43; DB 2; Length 78;  
 Best Local Similarity 77.8%; Pred. No. 18;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match Score 1 SVCCGYKLC 9  
 Best Local Similarity 77.8%; Pred. No. 18;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match Score 1 SVCCGQ--CYPC 23  
 Best Local Similarity 77.8%; Pred. No. 18;  
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

**RESULT 12**

A45910  
 ultra-high-sulfur keratin - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Accession: A45910  
 C;McNab, A.R.; Wood, L.; Theriault, N.; Gierman, T.; Vogeli, G.  
 J. Invest. Dermatol. 92, 263-266, 1989  
 A;Title: An ultra-high sulfur keratin gene is expressed specifically during hair growth.  
 A;Reference number: A45910; PMID: 89140394; PMID: 2465353  
 A;Accession: A45910  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Cross-references: GB:M27685; NID:9341749; PID:AAA81560.1; PMID:91066818  
 C;Superfamily: ultra-high-sulfur keratin

Query Match Score 54.4%; Score 43; DB 2; Length 186;  
 Best Local Similarity 60.0%; Pred. No. 34;  
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 CCGYKLCFPC 12  
 Db 42 CCGSSCCOPC 51

**RESULT 13**  
 T4487  
 Hypothetical protein F9K21.50 - *Arabidopsis thaliana*  
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
 R;Jordan, N.; Bangert, S.; Wiedelmann, R.; Voss, H.; Unseld, M.; Mewes, H.W.; Lemcke, K.  
 Submitted to the Protein Sequence Database, February 2000  
 A;Accession: Z24467  
 A;Accession: T4487  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-222 <JDR>  
 A;Cross-references: EMBL:AL138657  
 A;Experimental source: cultivar Columbia; BAC clone F9K21  
 C;Genetics:  
 A;Map position: 3  
 A;Introns: 186/2  
 A;Note: F9K21.50

Query	Match	Score	DB	Length
QY	4 CGYKLCFPC 12	54.4%	2	484
Db	187 CGQFCYKC 195	55.6%	2	66

Search completed: August 10, 2004, 16:04:57  
 Job time : 4.72973 SECS

---

QY 4 CGYKLCFPC 12  
 Db 187 CGQFCYKC 195

**RESULT 14**  
 E84647  
 Hypothetical protein At2g253360 [imported] - *Arabidopsis thaliana*  
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C;Accession: E84647  
 C;Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
 R;Lin, X.; Kaul, S.; Rounseley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
 euss, D.; Nieman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
 Nature 402, 761-768, 1999  
 A;Title: sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.  
 A;Accession number: A84420; PMID:20083487; PMID:10617197  
 A;Status: preliminary  
 A;Cross-references: GB:AE002093; NID:94432849; PIDN:AAD20697.1; GSPDB:GN00139  
 A;Gene: At2g253360  
 A;Molecule type: DNA  
 A;Residues: 1-373 <SNCO>  
 A;Map position: 2

Query	Match	Score	DB	Length
QY	4 CGYKLCFPC 12	54.4%	2	373
Db	273 CGQFCYQC 281	55.6%	2	60

**RESULT 15**  
 T20254  
 Hypothetical protein C55A6.1 - *Caenorhabditis elegans*  
 C;Species: *Caenorhabditis elegans*  
 C;Accession: T20254  
 C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 02-Sep-2000  
 R;Kershaw, J.  
 submitted to the EMBL Data Library, October 1996  
 A;Reference number: 219243

Scoring table:	BLOSUM62	Alignments
Gapop 10.0 , Gapext 0.5		
Searched:	141681 seqs., 52070155 residues	
Total number of hits satisfying chosen parameters:	141691	
Minimum DB seq length:	0	
Maximum DB seq length:	2000000000	
Post-processing:	Minimum Match 0%	
	Maximum Match 100%	
	Listing First 45 summaries	
Database :	SwissProt_42:*	
Pred. No.	Score	Query Match Length DB ID Description
1	68	86.1 11 1 CXL1 CONMR
2	68	86.1 13 1 CXL4 CONMR
3	68	86.1 61 1 CXL2 CONMR
4	54	68.4 12 1 CXL3 CONMR
5	50	63.3 55 1 MBAC DROME
6	47	59.5 245 1 IEG_NPYOP
7	44	55.7 342 1 YOT5_HAELIN
8	44	55.7 503 1 ART1_DROME
9	42.5	53.8 30 1 CKX4_CONST
10	42	53.2 434 1 ADK2_YEAST
11	41	51.9 235 1 YOT5_CABEL
12	41	51.9 539 1 RN37_MOUSE
13	41	51.9 541 1 RN37_HUMAN
14	41	51.9 1885 1 RRPO_ACLS
15	40	50.6 207 1 CSF3_HUMAN
16	40	50.6 452 1 RN18_HUMAN
17	40	50.6 566 1 IRRL_RAT
18	40	50.6 567 1 IRRL_MOUSE
19	40	50.6 575 1 YOT6_CABEL
20	40	50.6 4655 1 LRPL_HUMAN
21	39.5	50.0 1984 1 YL_DROME
22	39	49.4 208 1 CSF2_MOUSE
23	39	49.4 257 1 RFBF_SALTY
24	39	49.4 400 1 VGF9_HSV1
25	39	49.4 469 1 AR11_MOUSE
26	39	49.4 557 1 AR11_HUMAN
27	39	49.4 4543 1 LRPL_CHICK
28	39	49.4 4544 1 LRPL_HUMAN
29	38.5	48.7 92 1 NEU2_LOXAF
30	38.5	48.7 6781 1 R1AB_PEDV
31	38	48.1 72 1 YAU_VACC
32	38	48.1 232 1 SUT2_CABEL
33	38	48.1 261 1 MGR2_HUMAN
34		38 48.1 274 1 YEU6_YEAST
		35 38 48.1 321 1 ABVA_ASENG
		36 38 48.1 399 1 PEAC_YEAST
		37 38 48.1 408 1 VTN_NPVAC
		38 38 48.1 461 1 PRTC_HUMAN
		39 38 48.1 584 1 POTE_HUMAN
		40 38 48.1 653 1 HT2A_HUMAN
		41 38 48.1 685 1 MID2_MOUSE
		42 38 48.1 715 1 MID2_HUMAN
		43 38 48.1 775 1 CN04_MOUSE
		44 38 48.1 796 1 CN04_HUMAN
		45 38 48.1 872 1 MGR2_HUMAN

RN	[1] SEQUENCE, SYNTHESIS, AND STRUCTURE BY NMR.	RA Lewis R.J.;	RA "Two new classes of conopeptides inhibit the alpha1-adrenoceptor and
RP	PTISSUE=venom;	RT RT noradrenaline transporter;"	RT noradrenaline transporter;"
RC	MEDLINEB=21419681; PubMed=11528421;	RL Nat. Neurosci. 4:902-907(2001).	RL Nat. Neurosci. 4:902-907(2001).
RX	Sharpe I.A., Gehrmann J., Loughnan M.L., Adams D.A., Atkins A., Palant E., Craik D.J., Alewood P.F., Lewis R.J.;	CC -I- FUNCTION: Inhibits the neuronal noradrenaline transporter.	CC -I- FUNCTION: Inhibits the neuronal noradrenaline transporter.
RA	"Two new classes of conopeptides inhibit the alpha1-adrenoceptor and noradrenaline transporter.";	CC -I- SUBCELLULAR LOCATION: Secreted.	CC -I- SUBCELLULAR LOCATION: Secreted.
RA	Nat. Neurosci. 4:902-907(2001).	CC -I- TISSUE SPECIFICITY: Expressed by the venom duct.	CC -I- TISSUE SPECIFICITY: Expressed by the venom duct.
CC	-I- SIMILARITY: Belongs to the chi1/lambda-conotoxin family.	CC -I- PTM: Exists in two forms, due to cis-trans isomerization at His-59-Hyp-60.	CC -I- PTM: Exists in two forms, due to cis-trans isomerization at His-59-Hyp-60.
CC	-I- MASS SPECTROMETRY: MW=1408.5; METHOD=Electrospray.	CC -I- MASS SPECTROMETRY: MW=1408.5; METHOD=Electrospray.	CC -I- MASS SPECTROMETRY: MW=1408.5; METHOD=Electrospray.
CC	-I- SIMILARITY: Belongs to the chi1/lambda-conotoxin family.	CC -I- SIMILARITY: Belongs to the chi1/lambda-conotoxin family.	CC -I- SIMILARITY: Belongs to the chi1/lambda-conotoxin family.
DR	PDB; 1IBO; 03-APR-02.	DR InterPro; IPR04214; Conotoxin.	DR InterPro; IPR04214; Conotoxin.
KW	Neurotoxin; Toxin; Hydroxylation; 3D-structure.	KW Neurotoxin; Toxin; Hydroxylation; Signal.	KW Neurotoxin; Toxin; Hydroxylation; Signal.
CC	-I- PTM: Exists in two forms, due to cis-trans isomerization at His-11-Hyp-12.	FT SIGNAL 1 19 POTENTIAL.	FT SIGNAL 1 19 POTENTIAL.
CC	-I- MASS SPECTROMETRY: MW=1393.52; METHOD=Electrospray.	FT PROPEP 20 48	FT PROPEP 20 48
CC	-I- SIMILARITY: Belongs to the chi1/lambda-conotoxin family.	FT PEPTIDE 49 52	FT PEPTIDE 49 52
DR	PDB; 1IBO; 03-APR-02.	FT DISULFID 52 61	FT DISULFID 52 61
KW	Neurotoxin; Toxin; Hydroxylation; 3D-structure.	FT DISULFID 53 58	FT DISULFID 53 58
FT	DISULFID 4 13	FT MOD RES 60 60	FT MOD RES 60 60
FT	DISULFID 5 10	SQ SEQUENCE 61 AA; 6499 MW; F4E5B5A97EBBDBA CRC64;	SQ SEQUENCE 61 AA; 6499 MW; F4E5B5A97EBBDBA CRC64;
FT	MOD RES 12 12 HYDROXYLATION.	Query Match 86.1%; Score 68; DB 1; Length 61;	Query Match 86.1%; Score 68; DB 1; Length 61;
SQ	SEQUENCE 13 AA; 1382 MW; 27AAC376EAD2B58 CRC64;	Best Local Similarity 90.9%; Pred. No. 0.0006;	Best Local Similarity 90.9%; Pred. No. 0.0006;
Qy	2 VCCGYKLCPFC 12	Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Db	3 VCCGYKLCPFC 13	Db 51 VCCGYKLCPFC 12	Db 51 VCCGYKLCPFC 13
<b>RESULT 4</b>			
	CML3_CONMR	STANDARD;	STANDARD;
ID	CML3_CONMR	PRT;	PRT;
AC	P58809;	AC P58809;	AC P58809;
DT	28-FEB-2003 (Rel. 41, Created)	DT 28-FEB-2003 (Rel. 41, Created)	DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last sequence update)	DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE	Lambda-conotoxin CMrX.	DE Lambda-conotoxin CMrX.	DE Lambda-conotoxin CMrX.
OS	Conus marmoreus (Marble cone).	OS Conus marmoreus (Marble cone).	OS Conus marmoreus (Marble cone).
OC	Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda; Apogastropoda; Ctenogastropoda; Sorbeoconcha; Hypsogastropoda; Neogastropoda; Conoidea; Conidae; Conus.	OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda; Apogastropoda; Ctenogastropoda; Sorbeoconcha; Hypsogastropoda; Neogastropoda; Conoidea; Conidae; Conus.	OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda; Apogastropoda; Ctenogastropoda; Sorbeoconcha; Hypsogastropoda; Neogastropoda; Conoidea; Conidae; Conus.
RN	[1]	RN [1]; TaxID=42752;	RN [1]; TaxID=42752;
RP	SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.	RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.	RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC	PTISSUE=Venom;	RC PMID=10988292;	RC PMID=10988292;
RA	Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,	RA Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,	RA Balaji R.A., Ohtake A., Sato K., Gopalakrishnakone P., Kini R.M.,
RA	Seew K.T., Bay B.-H.;	RA Seew K.T., Bay B.-H.;	RA Seew K.T., Bay B.-H.;
RA	"Lambda-conotoxins, a new family of conotoxins with unique disulfide pattern and protein folding. Isolation and characterization from the venom of Conus marmoreus."	RA "Lambda-conotoxins, a new family of conotoxins with unique disulfide pattern and protein folding. Isolation and characterization from the venom of Conus marmoreus."	RA "Lambda-conotoxins, a new family of conotoxins with unique disulfide pattern and protein folding. Isolation and characterization from the venom of Conus marmoreus."
RA	J. Biol. Chem. 275:39516-39522(2000).	RA J. Biol. Chem. 275:39516-39522(2000).	RA J. Biol. Chem. 275:39516-39522(2000).
RA	-I- FUNCTION: Inhibits the neuronal noradrenaline transporter.	RA -I- FUNCTION: Inhibits the neuronal noradrenaline transporter.	RA -I- FUNCTION: Inhibits the neuronal noradrenaline transporter.
RA	-I- SUBCELLULAR LOCATION: Secreted.	RA -I- SUBCELLULAR LOCATION: Secreted.	RA -I- SUBCELLULAR LOCATION: Secreted.
RA	-I- TISSUE SPECIFICITY: Expressed by the venom duct.	RA -I- TISSUE SPECIFICITY: Expressed by the venom duct.	RA -I- TISSUE SPECIFICITY: Expressed by the venom duct.
RA	-I- SIMILARITY: Belongs to the chi1/lambda-conotoxin family.	RA -I- SIMILARITY: Belongs to the chi1/lambda-conotoxin family.	RA -I- SIMILARITY: Belongs to the chi1/lambda-conotoxin family.
RA	FT DISULFID 3 12	FT DISULFID 3 12	FT DISULFID 3 12
FT	DISULFID 4 9	FT DISULFID 4 9	FT DISULFID 4 9
SQ	SEQUENCE 12 AA; 1251 MW; 27AAE2422DSAC8 CRC64;	Query Match 68.4%; Score 54; DB 1; Length 12;	Query Match 68.4%; Score 54; DB 1; Length 12;
Qy	2 VCCGYKLCPFC 12	Best Local Similarity 54.5%; Pred. No. 0.016;	Best Local Similarity 54.5%; Pred. No. 0.016;
Db	2 ICCEVSFCPFC 12	Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;	Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

**RESULT 5**  
**M84C DROME STANDARD; PRT; 55 AA.**  
 AC Q01674; Q9VIA0;  
 DT 01-TUL-1993 (Rel. 26, Created)  
 DT 01-TUL-1993 (Rel. 26, Last sequence update)  
 DT 10-OCT-200 (Rel. 42, Last annotation update)  
 DE Male specific sperm protein Mst84C.  
 DE MST84DC OR CG17945.  
 OS Drosophila melanogaster (Fruit fly).  
 EUKARYOTA: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 Ephydriidea; Drosophilidae; Drosophila.  
 NCBI TaxID=7227;

[1] RP SEQUENCE FROM N.A.  
 RC STRAIN=Oregon-R;  
 RX MEDLINE=32102853; PubMed=1684716;  
 RA Kuhn R., Kuhn C.,  
 RA Schaefer M.;  
 RT "A cluster of four genes selectively expressed in the male germ line  
 of *Drosophila melanogaster*.";  
 RL Mech. Dev. 35:143-151(1991);  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC STRAIN=berkeley;  
 RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scheerer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazquez R.G., Champé M., Pfleiffer B.D., Wan K.H., Doyle C., Baxter F.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandaari D., Bolshakov S., Borukov D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cowley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A.D., Deng Z., Mays A.D., Dew I., Dietz S.M., Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin R.K.J., Evangelista C.C., Ferrara S., Fleischmann W., Fosler C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glaser K., Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M., Hostin N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L., Nelson D.M., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun B., Svartas R., Tector C., Turner R., Venter J.C., Wang A.H., Wang X., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*,"  
 Science 287:2185-2195(2000);  
 RL "Tissue specificity of primary spermatocytes."  
 CC "-!- TISSUE SPECIFICITY: Testis.  
 CC "-!- DEVELOPMENT STAGE: Primary spermatocytes.  
 CC "-!- DOMAIN: This protein is mostly composed of repetitive C-G-P motifs.  
 CC "-!- SIMILARITY: BELONGS TO THE MST (3)CGP FAMILY.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use by non-profit institutions as long as its content is in no way  
 CC modified and this statement is not removed. Usage by and for commercial  
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>).  
 CC or send an email to license@isb-sib.ch).

DR EMBL; X67703; CAA41939\_1/-;  
 DR AB003672; AAFA54055\_1/-;  
 DR PIR S25774; S25774;  
 DR Flybase; FBgn0004174; Mst84Dc.  
 DR InterPro; IPR005634; MSSP.  
 DR Pfam; PF33940; MSSP\_1.  
 KW Spermatogenesis; Repeat; Multigene family.  
 SQ SEQUENCE 55 AA; 5225 MW; 95A2F3AEC8BB06 CRC64;  
 SQ

Query Match	Score	DB 1;	Length
Best Local Similarity	63.3%	DB 1;	55;
Matches	70.0%	Pred. No.	0.25;
Conservative	0;	Mismatches	3;
		Indels	0;
		Gaps	0;

Qy 3 CCGYKLCFCPC 12  
 Db 9 CCGYTCGCP 18

**RESULT 6**  
**IEO\_NPVOPI NPVOPI STANDARD; PRT; 245 AA.**  
 ID IEO\_NPVOPI  
 ID NPVOPI  
 AC 010369;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Intermediate-early protein IE-0.  
 GN IE-0.  
 RA Rohrmann G.P.;  
 RA "The sequence of the *Orgyia pseudotsugata* multineucleocapsid nuclear polyhedrosis virus genome,"  
 RA Virology 222:381-399(1997).  
 CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/>) or send an email to license@isb-sib.ch).

CC DR EMBL; U75930; AAC59137\_1/-;  
 CC DR InterPro; IPR007954; BaculoIE-1.  
 CC DR InterPro; IPR001841; Znf\_ring.  
 CC DR Pfam; PF05290; BaculoIE-1.  
 CC DR PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
 CC DR PROSITE; PS50089; ZF\_RING\_2; 1.  
 CC DR Early\_Protein; Zinc\_Finger.  
 CC FT ZN\_FING 195 240 RING-TYPE.  
 CC SQ SEQUENCE 245 AA; 27117 MW; 35743B15F7B1029 CRC64;

Query Match	Score	DB 1;	Length
Best Local Similarity	59.5%	DB 1;	245;
Matches	60.0%	Pred. No.	2.7;
Conservative	1;	Mismatches	3;
		Indels	0;
		Gaps	0;

Qy 3 CCGYKLCFCPC 12  
 Db 213 CCQSYSLCYAC 222

RESULT 7  
 Y053\_HARIN STANDARD; PRT; 342 AA.  
 ID Y053\_HARIN STANDARD;  
 AC Q55177; (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-NOV-1997 (Rel. 42, Last annotation update)  
 DR Hypothetical zinc-type alcohol dehydrogenase-like protein HI0053.  
 GN HI0053.  
 OS Haemophilus influenzae.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;  
 OC Pasteurellaceae; Haemophilus .  
 CX NCBI\_TaxID=727;  
 RN [1]  
 RP SEQUENCE FROM N.A., STRAIN=K20 / ATCC 51907;  
 RXC MEDLINE=95350630; PubMed=7542800;  
 RA Flieischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.J.M., Keravage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., FitzHugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Utterback T.R., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Fine L.D., Fritchman J.L., Fuhrmann J.J.L., Geoghegan N.S.M., Graham C.L., McDonald L.A., Small K.V., Frazer C.M., Smith H.O., Venter J.C.; "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.", RD.; RT SCIENCE 269:496-512(1995).  
 CC -!- SIMILARITY: Binds 2 zinc ions per subunit (By similarity).  
 CC -!- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase family.  
 CC -!- This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).  
 CC -!- EMBL: AAC2731.1; DR 32690; AAC2731.1; -.  
 CC -!- PROTEIN: PS00059; ADH\_ZINC; FALSE\_NEG.  
 KW Hypothetical protein; Oxidoreductase; zinc; Metal-binding; Complete proteome.  
 FT METAL 41 41 ZINC 1 (CATALYTIC) (BY SIMILARITY).  
 FT METAL 63 63 ZINC 1 (CATALYTIC) (BY SIMILARITY).  
 FT METAL 94 94 ZINC 1 (CATALYTIC) (BY SIMILARITY).  
 FT METAL 97 97 ZINC 2 (BY SIMILARITY).  
 FT METAL 100 100 ZINC 2 (BY SIMILARITY).  
 FT METAL 108 108 ZINC 2 (BY SIMILARITY).  
 FT METAL 149 149 ZINC 1 (CATALYTIC) (BY SIMILARITY).  
 SQ SEQUENCE 342 AA; 37429 MW; 100B07F9194E694 CRC64;

Query Match 55.7%; Score 44; DB 1; Length 342;  
 Best Local Similarity 63.6%; Pred. No. 10;  
 Matches 7; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

Oy 2 VCCGYKCFPC 12  
 Db 92 VCCGQ-CYPC 100

ARI1\_DRONE STANDARD; PRT; 503 AA.  
 ID ARI1\_DRONE  
 AC Q99F61; (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 43, Last annotation update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Ariadne-1 protein (Ari-1).  
 GN Drosophila melanogaster (Fruit fly).  
 OS Drosophila melanogaster; Buiaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydrioidea; Drosophilidae; Drosophila. NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A., CHARACTERIZATION, AND MUTAGENESIS.  
 RC STRAIN=Oregon-R;  
 RX MEDLINE=20343325; PubMed=10880484;  
 RA Aguilera M., Oliveros M., Martinez-Padron M., Barbas J.A., Ferrus A.; "Ariadne-1: a vital Drosophila gene is required in development and defines a new conserved family of ring-finger proteins."; Genetics 155:1231-1244 (2000).  
 RN [2]  
 RP SEQUENCE FROM N.A., STRAIN=Berkley;  
 RX MEDLINE=20198006; PubMed=10731132;  
 RA Adams M.D., Celinski S.E., Holt R.A., Evans C.A., Gocayne J.D., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.R., Wortman J.M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazquez R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews P.-Fannikoch C., Baldwin D., Ballieu R.M., Basu A., Baxendale J., Bayraklaroglu L., Beasley E.M., Besson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borrova D., Botchan M.R., Bouck J., Brokstein P., Broctier P., Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Downes M., Dugan-Roche S., Dietz S.M., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Dunkov B.C., Ferreira S., Fleischmann R., Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibsegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., RA Kennison J.A., Ketchum K.A., Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milashina N.V., Mohr C., Morris J., Mosherfi A., Mount S.M., Moy M.M., Murphy L., Muzyk D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Pacile J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Sieden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svartkas R., Tector C., Turner R., Venter E., Wang A.H., Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhou W., Zhou X., Zhu S., Zhu X., Zulu G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195 (2000).  
 CC -!- FUNCTION: Might act as an E3 ubiquitin-protein ligase, or as part of E3 complex, which accepts ubiquitin from specific E2 ubiquitin-conjugating enzymes, such as UBCD10/UBE2L3, and then transfers it to substrate.  
 CC -!- SUBUNIT: Interacts with UBCD10. Can form dimers.  
 CC -!- SUBCELLULAR LOCATION: Mainly cytoplasmic.  
 CC -!- TISSUE SPECIFICITY: Widely expressed, with prominent levels in the nervous system and female gonads.  
 CC -!- DEVELOPMENTAL STAGE: Expressed in all tissues throughout

development, with maximum levels reached during metamorphosis and maintained in the adult.

-!- SIMILARITY: Contains 2 RING-type zinc fingers.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - use by non-profit institutions. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

EMBL: X98309; CAA66953\_1;  
 EMBL: X98310; CAA66954\_1.;  
 DR: BMBL; AE003507; AAF18807; 1.;  
 DR: Flybase; FBgn0017418; ari-1;  
 DR: PROSITE; PS00518; ZF\_RING\_2\_1;  
 DR: InterPro; IPR00067; Znf\_C6AC;  
 DR: InterPro; IPR0011841; Znf\_ring;  
 PFam: PF01485; IBR; 1;  
 SMART: SM00647; IBR; 2;  
 SMART: SM00184; RING; 2;  
 DR: PROSITE; PS00518; ZF\_RING\_1; FALSE\_NEG.  
 DR: PROSITE; PS50089; ZF\_RING\_2\_1;  
 Ubi conjugation pathway; Zinc-finger; Repeat; Coiled coil.  
 DOMAIN 22 27 ASP-RICH (ACIDIC).  
 FT ZN\_FING 133 182 RING-TYPE 1.  
 FT ZN\_FING 203 264 RING-TYPE 2.  
 FT ZN\_FING 291 336 RING-TYPE 3.  
 FT DOMAIN 133 201 INTERACTION WITH UBCD10.  
 FT MUTAGEN 341 361 COILED COIL (POTENTIAL).  
 FT MUTAGEN 150 150 C->Y: IN ARYL-2; LETHAL PHENOTYPE AND NO  
 FT MUTAGEN 309 309 LOSS OF INTERACTION WITH UBCD10.  
 FT MUTAGEN 55 68; 58932 MW; QAECC256CF5BC00 CRC64;

Query Match 55 7%; Score 44; DB 1; Length 503;  
 Best Local Similarity 55.6%; Pred. No. 14; Indels 0; Gaps 0;  
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 9  
 CKX4\_CONST CONST STANDARD PRT; 30 AA.  
 ID PS8921;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Kappa-A-conotoxin SIVA (Spastic peptide).  
 OS Conus striatus (Striated cone).  
 OC Apogastropoda; Gastropoda; Orthogastropoda; Hypsogastropoda;  
 Neogastropoda; Caenogastropoda; Sorbeconcha; Conidae; Conus.  
 RN [1] \_TAXID=6493;  
 RP TISSUE-venom;

RX MEDLINE=99036623; PubMed=9819194;  
 RA Craig A.G., Zafaralla G.C., Cruz L.J., Santos A.D., Hillyard D.R.,  
 RA Dykert J.J., Rivier J.E., Gray W.R., Imperial J.S., DelaCruz R.G.,  
 RA Sporning A., Terlau H., West P.J., Yoshihama D., Olivera B.M.,  
 RA "An O-glycosylated neurotoxin conus peptide.";  
 RA Biochemistry 37:16029-16025(1998);

-!- FUNCTION: Kappa-A-conotoxins bind and inhibit voltage-sensitive potassium channels. When injected intraperitoneally in fish, the peptide induces a period of rapid swimming followed by a spastic paralysis with stiff fibrillating fins. At high doses, the peptide is lethal to both fish and mice.

CC	-!- SUBCELLULAR LOCATION: Secreted.
CC	-!- TISSUE SPECIFICITY: Expressed by the venom duct.
CC	-!- PTM: O-linked glycan consists of Hex3-HexNAc2 disaccharide (probable).
CC	-!- MASS SPECTROMETRY: MN=4084.2; METHOD=LSIMS.
CC	-!- SIMILARITY: Belongs to the conotoxin O-superfamily.
KW	Toxin; Neurotoxin; Ionic channel inhibitor;
KW	Potassium channel inhibitor; Hydroxylation; Amidation;
KW	Pyridolidone carboxylic acid; Glycoprotein.
FT	DISULFID 12 24 PROBABLE.
FT	DISULFID 13 26 PROBABLE.
FT	DISULFID 21 30 PROBABLE.
CC	CC PROBABLE.
CC	CC PYRROLIDONE CARBOXYLIC ACID.
DR	CARBOHYD 1 1 O-LINKED.
FT	CARBOHYD 7 7 HYDROXYLATION.
FT	MOD_PBS 17 17 HYDROXYLATION.
FT	MOD_PBS 22 22 HYDROXYLATION.
FT	MOD_PBS 23 23 HYDROXYLATION.
FT	MOD_PBS 30 30 AMIDATION.
SQ	SEQUENCE 30 AA; 3166 MW; 758ACC1F146D7DS CRC64;
Query Match	53.8%; Score 42.5%; DB 1; Length 30;
Best Local Similarity	46.7%; Pred. No. 1.8%;
Matches	7; Mismatches 2; Indels 3; Gaps 1;
ADA2_YEAST	STANDARD; PRT; 434 AA.
AC	Q02336; ID:       :
DB	10 TTCCGYDPGTMCPPC 24
RESULT 10	SVCCSY---KLCFPC 12
ADA2_YEAST	ID:       :
AC	Q02336; ID:       :
DT	01-JUL-1993 (Rel. 26, Created)
DT	01-JUL-1993 (Rel. 26, Last sequence update)
DT	15-MAR-2004 (Rel. 43, Last annotation update)
DE	Transcriptional adapter 2.
GN	ADA2 OR YDR448W OR D9461-33.
OS	Saccharomyces cerevisiae (Baker's yeast).
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC	Saccharomyctaceae; Saccharomyctaceae; Saccharomyces.
[1]	NCBI_TaxID=4932;
RN	SEQUENCE FROM N.A.
RX	MEDLINE=92346713; PubMed=1638630;
RA	Berger S.L., Pina B., Silverman N., Marcus G.A., Agapite J.,
RA	Jacquier J., Alt-Moerbe J., Andre B., Ballesta J.P.G., Ballesta J.P.G.,
RA	Bargues M., Baron L., Becker A., Bitau N., Bloecker H., Blugeon C.,
RA	Boskovic J., Brundt P., Brueckner M., Buitrago M.J., Cootier F.,
RA	Delaveau T., del Rey J., Dujoj B., Eide D.G., Garcia-Cantalejo J.M.,
RA	Goffeau A., Gomez-Peris A., Granotier C., Hanemann V., Hankeln T.,
RA	Hoeftel J.D., Jaeger W., Jimenez A., Jonniaux J.-L., Kraemer C.,
RA	Kuester H., Lananen P., Legros Y., Louis E.J., Moeller-Rieker S.,
RA	Monnet A., Moro M., Mueller-Auer S., Nussbaumer B., Paricio N.,
RA	Paulin L., Perez J., Perez-Alonso M., Perez-Ortin J.E., Pohl T.M.,
RA	Prydz H., Puruelle B., Rasmussen S.W., Revuelta J.L.,
RA	Rieger M., Salom D., Saluz H.P., Saiz J.E., Saren A.-M., Schaefer M.,
RA	Scharte M., Schmidt B.R., Schneider C., Scholler P., Schwarz S.,
RA	Urrestarazu L.A., Verhaest P., Vissers S., Voet M., Volckaert G.,
RA	Wagner G., Wambell R., Wedler H.,
RA	Brown D., Chuncer C.M., Connor R., Dedman K., Gentles S.,
RA	Hamlin N., Hunt S., Jones L., McDonald S., Murphy L., Niblett D.,
RA	Odeil C., Oliver K., Rajandream M.A., Richards C., Shore L.,
RA	Walsh S.V., Barrell B.G., Dietrich F.S., Mulligan J.T., Allen E.,
RA	Araujo R., Aviles E., Beno A., Carpenter J., Chen E., Cherry J.M.,
RA	Chung E., Duncan M., Hunnicke-Smith S., Hyman R.W., Komp C.,

RA Lashkari D., Lew H., Lin D., Mosedale D., Nakahara K., Namath A., Nefner P., Oh C., Petel F.X., Roberts D., Schramm S., Schroeder M., Shoff N., Windt A., Yeltov M.A., Botstein D., Davis R.W., Johnson M., Andrews S.S., Brinkman R., Cooper J., Ding H., Du Z., Favelllo A., Fulcon L., Gattung S., Greco T., Hallsworth K., Hawks J., Hillier L.W., Jier M., Johnson D., Johnston L., Kirsten J., Kucaba T., Langston Y., Latreille P., Le T., Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D., Rikfin L., Riles L., Taich A., Traverski E., Vignati D., Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R., Albermann K., Hani J., Heumann K., Kleine K., Mewes H.-W., Zoller A., Zaccaria P.; "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome IV."; Nature 387:75-78 (1997). [3]

RN ASSOCIATION WITH GENES;  
RX MEDLINE=95043371; PubMed=7957049;  
RA Marcus G.A., Silverman N., Berger S.L., Horiuchi J., Guarante L.;  
RT "Functional similarity and physical association between GCN5 and ADA2: putative transcriptional adaptors.";  
RL EMBO J. 13:4807-4815(1994).

RN IDENTIFICATION IN A SAGA COMPLEX WITH SPT7; HFI1; SPT8; GCN5; SPT20;  
RP SPT2; ADA3 AND TRAI.  
RX MEDLINE=9102859; PubMed=9885573;  
RA Grant P.A., Schiebtz D., Pray-Grant M.G., Yates J.R. III,  
Workman J.L.;  
RA "The ATM-related cofactor Trai is a component of the purified SAGA complex.";  
RT Mol. Cell 2:863-867(1998).  
RL CC -I- FUNCTION: Required for the function of some acidic activation domains, which activate transcription from a distant site. The exact mechanism of action is not yet known. ADA2, ADA3 and GCN5 function to acetylate nucleosomes opening up the promoter region.  
CC -I- SUBUNIT: Interacts with GCN5. Part of the ADA/GCN5 complex that consists of HFI1/ADA1, ADA2, ADA3, SPT20/ADA5 and GCN5. Component of the SAGA complex, a large multiprotein complex that modifies the chromatin, at least composed of SPT2, SPT7, SPT8, SPT20/ADA5, HFI1, ADA2, ADA3/NGG1, TRAI and GCN5.  
CC -I- SUBCELLULAR LOCATION: Nuclear.  
CC -I- SIMILARITY: Contains 1 Myb-like domain.  
CC -I- SIMILARITY: Contains 1 SWIRM domain.  
CC -I- SIMILARITY: Contains 1 ZZ-type zinc finger.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).  
CC EMBL; SGD; S0002856; ADA2.  
DR Go; GO:0000124; C:SAGA complex; IDA.  
DR InterPro; IPR001005; Myb\_DNA\_binding.  
DR InterPro; IPR00526; SWIRM.  
DR InterPro; IPR00433; Znf\_ZZ.  
DR Germoline; 14040; -. [4]  
DR TRANSFAC; T02144; -. [4]  
DR SMART; SM0059; SANT; 1.  
DR SMART; SM00717; SANT; 1.  
DR SMART; SM00291; Znf\_ZZ; 1.  
DR PROSITE; PS00037; MYB\_1; FALSE\_NEG.  
DR PROSITE; PS00334; MYB\_2; FALSE\_NEG.  
DR PROSITE; PS00090; MYB\_3; 1.  
DR PROSITE; PS50934; SWIRM; 1.  
DR PROSITE; PS50135; ZF\_ZZ\_1; 1.  
DR PROSITE; PS50135; ZF\_ZZ\_2; 1.  
DR Transcription regulation; Zinc-finger.

FT ZN\_FING 1 48 ZZ-TYPE.  
FT DNA\_BIND 65 108 MYB\_SWIRM.  
SQ SEQUENCE 434 AA; 50569 MW; 9637E1EDBBBD0AC3 CRC64;

Query Match 53.2%; Score 42; DB 1; Length 434;  
Best Local Similarity 50.0%; Pred. No. 25;  
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SVCGCYKLFCFPC 12  
Db ::| | | | |  
23 AICPEYDLCVPC 34

RESULT 11  
YQ57CAEEL STANDARD; PRT; 235 AA.  
ID YQ57CAEEL  
AC Q09463;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hypothetical RING finger protein C16C10.7 in chromosome III.  
GN C16C10.7.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peleoderrinae; Caenorhabditis.  
OC NCBITaxID=6239;  
OX [1] -  
RN [1] -  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2;  
RA Lloyd C.;  
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.  
CC -1 SIMILARITY: Contains 1 RING-type zinc finger.  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).  
CC EMBL; Z46787; CAA85745; 1; -  
DR PIR; T19328; T19328.  
DR WormPep; C16C10.7; CB01438.  
DR InterPro; IPR001841; Znf\_ring.  
DR SMART; SM00184; ZF-C3HC4; 1.  
DR PROSITE; PS00518; ZF\_RING\_1; 1.  
DR PROSITE; PS50089; ZF\_RING\_2; 1.  
KW Hypothetical protein\_Zinc-finger.  
FT ZN\_FING 26 67 RING-TYPE.  
FT DOMAIN 121 124 POLY-GLY.  
FT DOMAIN 169 172 POLY-ALA.  
SQ SEQUENCE 235 AA; 24915 MW; 21A04AE951F6382A CRC64;

Query Match 51.9%; Score 41; DB 1; Length 235;  
Best Local Similarity 55.8%; Pred. No. 20;  
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 CGYKLCFPC 12  
Db 41 CSHLFCVPC 49

RESULT 12  
RN37\_MOUSE STANDARD; PRT; 539 AA.  
ID RN37\_MOUSE  
AC Q525F4;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Ring finger protein\_37 (Ubiquitin conjugating enzyme 7 interacting

DE	protein 5) (ubcm4 interacting protein 5).
GN	RNP37 OR UBC71P5 OR UIP5.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NCBI_TAXID	10090;
RN	[1]
SEQUENCE FROM N.A.	
RX	Medline:2126466; PubMed=11274149;
RA	Pringa E., Martinez-Noel G., Muller U., Harbers K.;
RT	"Interaction of the RING finger-related U-box motif of a nuclear dot protein with ubiquitin-conjugating enzymes.";
RL	J. Biol. Chem. 276:19617-19623 (2001).
[2]	
RP	SEQUENCE FROM N.A.
RC	TISSUE-Kidney;
RX	Medline:22388257; PubMed=12477932;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.E., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Matsunaga K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loguelino N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Richards S., Worley K.C., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muniz D.M., Sodergren E.J., Lu X., Gibbs R.A., Whiting M., Heaton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G., Rodriguez A.C., Grimes J.W., Green B.D., Dickson M.C., Butterfield Y.S.N., Krzywinski M.I., Skalnik D.E., Schnerer A., Schein J.E., Jones S.J.M., Marra M.A.; RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
RA	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC	--SUBUNIT: Interacts with UBE2J3.
CC	--SIMILARITY: Contains 1 RING-type zinc finger.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch">http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch</a> ).
CC	EMBL: AF360997; AAC51467.1; PROSITE: PS00518; AAH25068.1; DR MGI: 2154658; Rnf57; DR InterPro: IPR003613; Znf_modRing; DR InterPro: IPR001841; Znf_ring; PFam: PF04564; U-box: 1. SMART: SM00184; RING: 1. SMART: SM00504; Ubox: 1. DR PROSITE: PS00518; ZF_RING_1; DR PROSITE: PS050089; ZF_RING_2; DR Ubl conjugation pathway; Zinc-finger. KW DOMAIN 263 331 UBOX. FT ZN FING 481 526 RING-TYPE. FT CONFLICT 75 75 Y -> C (IN REF. 2). SQ SEQUENCE 539 AA; 58731 MW; 93F7372A92888814 CRC64;
Query Match	Score 41: DB 1; Length 539;
Best Local Similarity	51.9%;
Matches	66.7%;
Qy	CGYKLCFC 12
Dy	:       CGHLLCRDC 510
RN	STANDARD; PRT; 541 AA.
ID	034941;
AC	AC
DT	28-FEB-2003 (Rel. 41, Created)
DT	28-FEB-2003 (Rel. 41, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Ring finger protein 37 (Ubiquitin conjugating enzyme 7 interacting protein 5).
GN	RNP37 OR UBC71P5 OR KIAA0860.
OS	Homo sapiens (Human).
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
NCBI_TAXID	9666;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE-Brain;
RX	Medline:99156230; PubMed=10048485;
RA	Nagase T., Ishikawa K.-I., Suyana M., Kikuno R., Hiroshima M., Miyajima N., Tanaka A., Kocami H., Nomura N., Ohara O.; RT "Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";
RT	RT
RL	RT
RN	DNA Res. 5:355-364 (1998).
[2]	
RP	SEQUENCE FROM N.A.
RX	Medline:21638749; PubMed=11780052;
RA	Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R., Jones M., Steavens G., Babbage A.K., Baggaley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J., Buck D., Burall W.D., Butler A.P., Carter C., Carter N.P., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Cleo C.M., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Grahame D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Hartley J.L., Holden J.D., Holden P.J., Hucke B., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Lehaevesiaino M.H., Leverkus M.A., Lloyd C., Lovell J.D., Marsh V.L., Martin S.L., McConnachie L.J., McHurray A.A., Milne S.A., Misery D., Moore M.J.F., Mulligan J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.T., Phillipmore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showken R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whitehead S.J., Whitaker T., Willey D.L., Williams J., Williams S.A., Wilmung L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.; RT "The DNA sequence and comparative analysis of human chromosome 20.";
RL	Nature 414:865-871 (2001).
RN	[3]
RP	SEQUENCE FROM N.A.
RC	TISSUE-Lung;
RX	Medline:22388257; PubMed=12477932;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Marusina K., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Soares M.B., Bonaldo M.F., Cassavant T.L., Schaeetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mulahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Guraratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gey L.J., Hulyk S.W., Villacon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahay J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krywienski M.I., Skaltsa U., Smailus D.E., Schmer A., Schein J.E., Jones S.J.M., Marrs M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; <i>Proc. Natl. Acad. Sci. U.S.A.</i> 99:16899-16903 (2002).	CC entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
RT -!- SUBUNIT: Interacts with UBE2L3 (By similarity).	CC
CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).	CC
CC -!- SIMILARITY: Contains 1 RING-type zinc finger.	CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	CC
DR EMBL; AB020667; BAA74883.1; -;	DR
DR EMBL; AU121891; CAC09903.1; -;	DR
DR EMBL; BC000515; AAH00515.1; -;	DR
DR InterPro; IPR003613; Zinc_finger.	DR
DR InterPro; IPR001841; Zinc_finger.	DR
DR Pfam; PF04564; U-pox_1.	DR
DR SMART; SM00184; RING_1.	DR
DR PROSITE; PS00504; Ubiquitin.	DR
DR PROSITE; PS00518; ZF_RING_1_1.	DR
DR Ubl conjugation pathway; Zinc-finger; Nuclear protein.	DR
KW DOMAIN_263	KW
FT 331	FT
ZN FINGER_483	FT
RING_TYPE_528	FT
SEQUENCE_541 AA; 58965 MW; 4AF1AOCS115FAF7B CRC64; 504 CGHLICRPC 512	SEQUENCE
Query Match Score 41; DB 1; Length 541; Best Local Similarity 51.9%; Pred. No. 43; Mismatches 2; Indels 0; Gaps 0; Matches 6; Conservative	Query Match Score 41; DB 1; Length 1885; Best Local Similarity 51.9%; Pred. No. 1.3e+02; Mismatches 2; Indels 6; Gaps 1; Matches 15
Db	Db
RESULT 14	RESULT 15
RRPO_ACLSA ID _RRPO_ACLSA STANDARD; PRT; 1885 AA.	CSF3_HUMAN ID _CSF3_HUMAN STANDARD; PRT; 207 AA.
AC P54791; DR -!- 1996 (Rel. 34, Created)	AC P09919; DR -!- 1989 (Rel. 10, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)	DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)	DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE RNA-directed RNA polymerase (EC 2.7.7.48) (RNA replicase) (216.5 kDa protein) (ORF1).	DE Granulocyte colony-stimulating factor precursor (G-CSF) (Pluripotetin)
DE protein (ORF1).	DE (Fibrigrastim) (Lenograstim).
OS Apple chlorotic leaf spot virus (isolate apple) (ACLSV).	OS Homo sapiens (Human).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flexiviridae; Trichovirus.	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=73472;	OX NCBI_TaxID=9606;
RN SEQUENCE FROM N.A. MEDLINE=93389448; PubMed=8376968;	RN SEQUENCE FROM N.A. MEDLINE=86118679; PubMed=3484805;
RA Sato K., Yoshikawa N., Takahashi T.; "Complete nucleotide sequence of the genome of an apple isolate of apple chlorotic leaf spot virus." ; J. Gen. Virol. 74:1927-1931 (1993).	RA Nagata S., Tauchiya M., Asano S., Kaziro Y., Yamamoto O., Hirata Y., Kubota N., Oheda M., Nomura H., Ono M.; "Molecular cloning and expression of cDNA for human granulocyte colony-stimulating factor." ; Nature 319:415-418 (1986).
RL [1]	RL [2]
RR SEQUENCE FROM N.A. MEDLINE=86220137; PubMed=2423327;	RR SEQUENCE FROM N.A. MEDLINE=81196336; PubMed=3494801;
RA Nagata S., Tauchiya M., Asano S., Yamamoto O., Hirata Y., Kubota N., Nomura H., Yamazaki T.; "The chromosomal gene structure and two mRNAs for human granulocyte colony-stimulating factor." ; EMBO J. 5:575-581 (1986).	RA Devlin J.J., Devlin P.E., Myambo K., Lilly M.B., Rado T.A., Warren M.K.; "Expression of granulocyte colony-stimulating factor by human cell lines." ; J. Leukoc. Biol. 41:302-306 (1987).
RL [3]	RL [4]
RR SEQUENCE FROM N.A. MEDLINE=81196336; PubMed=3494801;	RR SEQUENCE FROM N.A. MEDLINE=86220137; PubMed=2423327;
RA Nagata S., Tauchiya M., Asano S., Yamamoto O., Hirata Y., Kubota N., Nomura H., Yamazaki T.; "The chromosomal gene structure and two mRNAs for human granulocyte colony-stimulating factor." ; EMBO J. 5:575-581 (1986).	RA Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q., Nickerson D.A.; "Expression of granulocyte colony-stimulating factor by human cell lines." ; J. Leukoc. Biol. 41:302-306 (1987).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	CC
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate + (RNA) (N).	CC
CC -!- SIMILARITY: TO THE PUTATIVE REPLICATION-ASSOCIATED PROTEINS OF POTEXVIRUSES.	CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).	CC
CC Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.	CC

[5] RN SEQUENCE OF 19-207 FROM N.A.  
RX MEDLINE=86151694; PubMed=2420009;  
RA Souza L.M., Boone T.C., Gabrilove J., Lai P.H., Zsebo K.M.,  
RA Murdock D.C., Chazin V.R., Bruszewski J., Lu H., Chen K.K.,  
RA Barndt J., Platzer E., Moore M.A.S., Mertelsmann R., Welte K.;  
RT "Recombinant human granulocyte colony-stimulating factor: effects on  
normal and leukemic myeloid cells.";  
RL Science 232:61-66 (1986).  
RN [6]  
RP CARBOHYDRATE-LINKAGE SITE.  
RX MEDLINE=92293942; PubMed=7685769;  
RA Clogston C.L., Hu S., Boone T.C., Lu H.S.;  
RT "Glycosidase digestion, electrophoresis and chromatographic analysis  
of recombinant human granulocyte colony-stimulating factor glycoforms  
produced in Chinese hamster ovary cells.";  
RL J. Chromatogr. A 637:55-62 (1993).  
RN [7]  
RP STRUCTURE BY NMR.  
RX MEDLINE=93106200; PubMed=1281794;  
RA Zink T., Ross A., Ambrosius D., Rudolph R., Holak T.A.;  
RT "Secondary structure of human granulocyte colony-stimulating factor  
derived from NMR spectroscopy.";  
RL FEBS Lett. 314:435-439 (1992).  
RN [8]  
RP STRUCTURE BY NMR.  
RX MEDLINE=94304859; PubMed=7518249;  
RA Zink T., Ross A., Luers K., Cieslar C., Rudolph R., Holak T.A.;  
RT "Structure and dynamics of the human granulocyte colony-stimulating  
factor determined by NMR spectroscopy. Loop mobility in a four-helix-  
bundle protein";  
RL Biochemistry 33:8453-8463 (1994).  
RN [9]  
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).  
RX MEDLINE=93281718; PubMed=935117;  
RA Hill C.P., Osslund T.D., Eisenberg D.;  
RT "The structure of granulocyte-colony-stimulating factor and its  
relationship to other growth factors.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:5167-5171 (1993).  
CC -!- FUNCTION: GRANULOCYTE/MACROPHAGE COLONY-STIMULATING FACTORS ARE  
CC CYTOKINES THAT ACT IN HEMATOPOIETIC CELLS BY CONTROLLING THE PRODUCTION,  
CC DIFFERENTIATION, AND FUNCTION OF 2 RELATED WHITE CELL POPULATIONS  
CC OF THE BLOOD, THE GRANULOCYTES AND THE MONOCYTES-MACROPHAGES. THIS  
CC CSF INDUCES GRANULOCYTES.  
CC -!- SUBUNIT: Monomer.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=Long;  
CC IsoId=P09919-1; Sequence=Displayed;  
CC Name=Short;  
CC IsoId=P09919-2; Sequence=TSP 002673;  
CC -!- PTM: O-SHGLYCAN CONSISTS OF GAL-GALNAc DISACCHARIDE WHICH CAN BE  
CC MODIFIED WITH UP TO TWO SIALIC ACID RESIDUES (DONE IN  
CC RECOMBINANTLY EXPRESSED G-CSF FROM CHO CELLS).  
CC -!- PHARMACEUTICAL: Available under the names Neupogen or Granulokine  
CC (Amgen/Roche) and Granocyte (Rhone-Poulenc). Used to treat  
CC neutropenia (a disorder characterized by an extremely low number  
CC of neutrophils in blood).  
CC -!- SIMILARITY: Belongs to the IL-6 superfamily.  
CC -!- CAUTION: REF 4 MISQUOTE THE GENE NAME AS "CSF1".  
CC -!- DATABASE: NAME=Neupogen/Granulokine;  
CC NOTE=Clinical information on Neupogen/Granulokine;  
CC WWW="http://www.neupogen.com/".

DR EMBL; X03438; CAA27168.1; -;  
DR EMBL; M13008; AAA001056.1; -;  
DR EMBL; X03656; CAA27291.1; -;  
DR EMBL; X03655; CAA27290.1; -;  
DR EMBL; AF88025; AAC62469.1; -;  
DR EMBL; M17705; AAA35882.1; -;  
DR PIR; A24573; AAC4573.1;  
DR PIR; A25093; P0HUGL;  
DR PDB; 1RHG; 31-JAN-94;  
DR PDB; 1GNC; 31-JUL-94;  
DR PDB; 1CD9; 08-MAR-00;  
DR PDB; 1PGR; 08-MAR-00;  
DR Genew; HGNC; 24338; CSF3.  
DR MIM; 138970; -;  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0005130; F:granulocyte colony-stimulating factor recep. - ; TAS.  
DR GO; GO:0007275; P:development; TAS.  
DR InterPro; IPR003629; GCSF MGF.  
DR InterPro; IPK003573; IL6\_MGF\_GCSF.  
DR Pflan; P00489; IL6; 1.  
DR PRINTS; PR00433; IL6GCSFMGFG.  
DR ProDom; PD000388; GCSF\_MGF; 1.  
DR SMART; SM0126; IL6; 1.  
DR PROSITE; PS00254; INTERLEUKIN\_6; 1.  
KW Cytokine; Growth factor; Glycoprotein; Signal; Alternative splicing;  
KW Polymorphism; Pharmaceutical; 3D-structure.  
KW FT SIGNAL; 1 30  
KW FT CHAIN 31 207  
FT DISULFID 69 75  
FT DISULFID 97 107  
FT CAREOHYD 166 166  
FT VARSPPLIC 66 68  
FT FT Missing (in Isoform Short). /FTID=VSP\_002673.  
FT CHAIN 31 207  
FT FT GRANULOCYTE COLONY-STIMULATING FACTOR.  
FT FT DISULFID 69 75  
FT FT DISULFID 97 107  
FT FT CAREOHYD 166 166  
FT FT O-LINKED (GALNAc. - ) (BY SIMILARITY). /FTID=VAR\_013073.  
FT FT VARIANT 157 157  
FT FT VARIANT 157 157  
FT FT VARIANT 174 174  
FT FT VARIANT 174 174  
FT HELIX 41 65  
FT HELIX 69 71  
FT HELIX 77 85  
FT TURN 87 88  
FT HELIX 105 124  
FT TURN 125 127  
FT TURN 130 132  
FT HELIX 133 156  
FT TURN 157 158  
FT HELIX 176 203  
FT TURN 204 204  
SQ SEQUENCE 207 AA; 22293 MW; 421F635ECC776996 CRC64;  
Query Match 50.6%; Score 40; DB 1; Length 207;  
Best Local Similarity 63.6%; Pred. No. 25;  
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 SVCCGYKLCPF 11  
Db 67 SBCATYKLCHP 77

Search completed: August 10, 2004, 16:03:05  
Job time : 3.59459 secs

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

Black Gheet

Result No.	Score	Match Length	DB ID	Description
1	63	79.7	64	Q9BPB9 conus peana
2	54	68.4	244	Q9IBQ9 spodoptera
3	53	67.1	243	Q80LS1 adoxophyes
4	53	67.1	258	Q36453 lymantria d
5	52	65.8	446	Q96BQ3 homo sapien
6	50	63.3	151	Q10614 helicoverpa
7	50	63.3	285	Q8V5X4 helicoverpa
8	50	63.3	285	Q99H38 helicoverpa
9	50	63.3	514	Q9LD86 arabidopsis
10	49	62.0	428	Q9M2P5 arabidopsis
11	49	62.0	436	Q8RXP2 arabidopsis
12	48	60.8	2259	Q7XIF9 oryza sativ
13	47	59.5	373	Q9m1F9 arabidopsis
14	47	59.5	470	Q9FWW3 arabidopsis
15	47	59.5	525	Q9LEB5 arabidopsis
16	47	59.5	641	Q9HJH7 thermoslas

Q91BQ9	PRELIMINARY;	PRT;	244 AA.	DR GO:0006118; P:electron transport; IEA.
AC Q91BQ9;				DR InterPro; IPR007956; CrtC_heme_Bs.
DT 01-OCT-2000 (TREMBLrel. 15, Created)				DR InterPro; IPR000345; CrtC_heme_Bs.
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)				DR InterPro; IPR001841; Znf_ring.
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)				PFam; PF05290; BaculoIE-1; 1.
DE ORF138 ie0.				DR PROSITE; PS00190; CYTOCHROME_C; 1.
OS Spodoptera exigua nucleopolyhedrovirus.				DR PROSITE; PS50089; ZF_RING_2; 1.
OC dsDNA viruses, no RNA stage; Baculoviridae;				DR PROSITE; PS50089; ZF_RING_2; 1.
OC Nucleopolyhedrovirus.				SEQUENCE 243 AA; 28756 MN; SD72075190E974A5 CRC64;
OX NCBI_TaxID=1054;				
RN [1]				Query Match 67.1%; Score 53; DB 12; Length 243;
RP PARTIAL SEQUENCE FROM N.A.				Best Local Similarity 60.0%; Pred. No. 0.6;
RX MEDLINE=97437494; PubMed=9292027;				Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
RA van Strien E.A., Faktor O., Hu Z.H., Zuidema D., Goldbach R.W., Vlak J.M.; "Baculoviruses contain a gene for the large subunit of ribonucleotide reductase.", RT				
RA J. Gen. Virol. 78:2365-2377(1997).				
RN [2]				
RP SEQUENCE FROM N.A.				RESULT 4
RX MEDLINE=20036646; PubMed=10567663;				O36453 PRELIMINARY;
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				ID O36453 ; Q9YMF3 ; AC 036453 ; Q9YMF3 ; DT 01-JAN-1998 (TREMBLrel. 05, Created)
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				DB Immediate early 0 protein (immediate early transactivator 0).
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				GN IE-0.
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				LYmantria dispar multicapsid nuclear polyhedrosis virus (LdMNPV).
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				OS Viruses; dsDNA viruses, no RNA stage; Baculoviridae.
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				OC Nucleopolyhedrovirus.
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				NCBI_TaxID=10449;
RN [3]				RN [1]
RP SEQUENCE FROM N.A.				RP SEQUENCE FROM N.A.
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				RX MEDLINE=97445058; PubMed=9300047;
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				RA Pearson M.N., Rohrmann G.F.;
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				RT "Splicing is required for transactivation by the immediate early gene 1 of the Lymantria dispar multicapsid nuclear polyhedrosis virus."
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				RT Virusology 235:153-165 (1997).
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				RL Virology 253:17-34 (1999).
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				RN [2]
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				RP SEQUENCE FROM N.A.
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				RA Kurzlo J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T., Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				RN [3]
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				RP SEQUENCE FROM N.A.
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				RA Kurzlo J., Pearson M.N., Harwood S.H., Funk C.J., Evans J.T., Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				RN [4]
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				RP SEQUENCE FROM N.A.
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				RA Kurzlo J.; Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				DR EMBL; AF06636; AAC58234.1; -.
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				DR PIR; T30368; T30368.
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				DR InterPro; IPR007954; BaculoIE-1.
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				DR InterPro; IPR001841; Znf_ring.
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				DR PFam; PF05290; BaculoIE-1.
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				DR SMART; SM00184; RING_1.
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				DR PROSITE; PS50089; ZF_RING_2; 1.
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				SQ SEQUENCE 258 AA; 2995 MN; AC564CDF92228BAD CRC64;
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				Query Match 67.1%; Score 53; DB 12; Length 258;
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				Best Local Similarity 58.3%; Pred. No. 0.63;
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				QY 1 SVCGYKLICFPC 12
RA IJKEK W.P.J., van Strien E.A., Heldens J.G., Broer R., Zuidema D., Goldbach R.W., Vlak J.M.; "Sequence and organization of the spodoptera exigua multicapsid nucleopolyhedrovirus genome.", RT				Db 207 NVCCGYRVNAC 218

RESULT 5	DR PROSITE; PS50089; ZF RING_2; 1.
Q96BQ3	SQ SEQUENCE 151 AA; 17548 MW; 4986432F6DCD3169 CRC64;
ID Q96BQ3 ; PRELIMINARY;	Query Match 63.3%; Score 50; DB 12; Length 151;
AC Q96BQ3 ;	Best Local Similarity 70.0%; Pred. No. 1.2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)	Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)	
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
DE Hypothetical protein.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX NCBI_TaxID=9606 ;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC TISSUE-Placenta;	
RA Strasbourg R.;	
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.	
CC  - SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.	
DR EMBL; BC01535; AAH1535.1; -.	
DR GenBank; RGNC:19015; TRIM43.	
DR GO:0005622; Cintacellular; IEA.	
DR GO:0008270; Zinc ion binding; IEA.	
DR InterPro; IPR001870; B302.	
DR InterPro; IPR003877; SPRY receptor.	
DR InterPro; IPR00315; Znt_Bbox.	
DR InterPro; IPR001841; Znf_ring.	
DR Pfam; PF00622; SPRY; 1.	
DR Pfam; PF00643; zf-B_box; 1.	
DR SMART; SM00184; zf-C3HC4; 1.	
DR PROSITE; PS50119; ZF_BBOX; 1.	
DR PROSITE; PS00518; ZF_RING_1; 1.	
DR PROSITE; PS50089; ZF_RING_2; 1.	
XW Hypothetical protein; Metal-binding; Zinc-finger.	
SEQUENCE 446 AA; 52265 MW; 805E4AA25617724A CRC64;	
Query Match 65.8%; Score 52; DB 4; Length 446;	
Best Local Similarity 50.0%; Pred. No. 1.4;	
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;	
Qy 1 SVCGYKLCFPC 12	Query Match 63.3%; Score 50; DB 12; Length 285;
Db 27 TICGGHSRPRC 38	Best Local Similarity 70.0%; Pred. No. 2.1;
	Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
RESULT 6	
O10614	DR PROSITE; PS50089; ZF RING_2; 1.
ID O10614 ; PRELIMINARY;	Query Match 63.3%; Score 50; DB 12; Length 285;
AC O10614 ;	Best Local Similarity 70.0%; Pred. No. 2.1;
DT 01-JUL-1997 (TREMBLrel. 04, Created)	Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)	
DE ACMNPV homolog.	
OS Helicoverpa zea single nucleocapsid nucleopolyhedrovirus.	
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;	
OC Nucleopolyhedrovirus.	
OX NCBI_TaxID=10468 ;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;	
RA Tribe D.;	
RT "Genetically variable triple repeats in a RING-finger ORF of Helicoverpa species baculoviruses.";	
RT Virus Res 49:67-77(1997).	
RL Virus Res 49:67-77(1997).	
DR EMBL; U67264; AAB5405.1; -.	
DR InterPro; IPR007954; Baculo IE-1.	
DR InterPro; IPR001841; Znf_ring.	
DR Pfam; PF05290; Baculo IE-1; 1.	
SMART; SM00184; RING; 1.	
RN [2]	
RP SEQUENCE FROM N.A.	
RC SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;	
RA Deng F., Chen X., Vlak J.M., Arif B.M., Hu Z.;	
RT "Sequence analysis of the gp37 gene of Heliothis armigera single-	
RT nucleocapsid nucleopolyhedrovirus.";	
RL Zhongguo Bingduixue 15:35-42(2000).	
RN [2]	
RP SEQUENCE FROM N.A.	
RC SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;	
RA Wang H., Hu Z., Sun X., Vlak J.M., Chen X.;	
RT "Sequence analysis of the iap3 gene of Heliothis armigera single-	

[1] SEQUENCE FROM N.A.  
SPECIES=Helicoverpa armigera nucleopolyhedrovirus ;  
MEDLINE=21078300; PubMed=11210394;  
Wang H., Chen X., Wang H., Arif B.M., Vlak J.M., Hu Z.;  
"Nucleotide sequence and transcriptional analysis of a putative basic  
DNA-binding protein of Helicoverpa armigera polyhedrovirus.";  
Virus Genes 22:113-120(2001).  
[4]

[5] SEQUENCE FROM N.A.  
SPECIES=Helicoverpa armigera nucleopolyhedrovirus G4;  
MEDLINE=21064569; PubMed=11215177;  
Chen X., Ijkel W.F., Tarchini R., Sun X., Sandbrink H., Wang H.,  
Peters S., Zuidema D., Lankhorst R.K., Vlak J.M., Hu Z.;  
"The sequence of the Helicoverpa armigera single-nucleocapsid  
nucleopolyhedrovirus genome.";  
J. Gen. Virol. 82:241-257(2001).  
[6] SEQUENCE FROM N.A.  
SPECIES=Helicoverpa armigera nuclear polyhedrosis virus; STRAIN=C1;  
PubMed=12030807;  
Zhang C.X., Wu J.C.;  
"Genome structure and the p10 gene of the Helicoverpa armigera  
nucleopolyhedrovirus";  
Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 33:179-184(2001).  
[7] SEQUENCE FROM N.A.  
SPECIES=Helicoverpa armigera nuclear polyhedrosis virus; STRAIN=C1;  
Zhang C.X., Jin W.R.,  
Submitted [SEB-2000] to the EMBL/GenBank/DBJ databases.  
[8] SEQUENCE FROM N.A.  
SPECIES=Helicoverpa armigera nuclear polyhedrosis virus; STRAIN=C1;  
PubMed: AF271059; AAC53751.1;  
EMBL: AF303045; AAK96301.1; -;  
InterPro: IPR007934; Baculo\_IIE-1.  
InterPro: IPR001641; Znf\_fing.  
PFAM: PF05290; Baculo\_IIE-1; 1.  
SMART: SM00184; RING; 1.  
PROSITE: PS50089; ZF\_RING\_2; 1.  
SEQUENCE 285 AA; 33186\_MW; C5FC3AAB65BA27BDD CRC64;

Query Match 63.3%; Score 50; DB 12; Length 285;  
Best Local Similarity 70.0%; Pred. No. 2.1;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps

99LD86 PRELIMINARY; PRT; 514 AA.  
99LD86  
01-OCT-2000 (TREMBL) 15, Created)  
01-OCT-2000 (TREMBL) 15, Last sequence update)  
01-OCT-2003 (TREMBL) 25, Last annotation update)

3 CCGYKLCFPC 12  
235 CCGYKICNLIC 244

RESULT 9  
99LD86 PRELIMINARY;  
99LD86  
01-OCT-2000 (TREMBL) 15, Created)  
01-OCT-2000 (TREMBL) 15, Last sequence update)  
01-OCT-2003 (TREMBL) 25, Last annotation update)

DE Hypothetical protein.  
AR4G11390  
DS Anthonomus thalana (Mouse-ear cress);  
Eukaryota; Viridiplantae; Strptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
euRosids II; Brassicales; Brassicaceae; Arabidopsis;  
NCBI\_TaxID=3702;  
[1] SEQUENCE OF 1-167 FROM N.A.  
RP Bevan M., Robben J., Grumontprez B., Volckaert G., Bancroft I.,



[1] RN SEQUENCE FROM N.A.  
 RP Fedderspiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F.,  
 RA Altai H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S.,  
 RA Buehler E., Chao Q., Chin C., Choi B., Gonzalez A.,  
 RA Howng B., Johnson-Hanson C., Khan S., Kim C., Koo T., Lee J.M.,  
 RA Lenz C., Liu A., Liu S., Mukharsky N., Pham P., Sakano H., Shinn P.,  
 RA Toriumi M., Vayberg M., Yu G.,  
 RA Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.  
 RL DR BMBL; AC022522; AAG1580.1; -.  
 DR PIR; C86256; C86256.  
 DR GO; GO:0015036; F:disulfide oxidoreductase activity; IEA.  
 DR GO; GO:0004497; F:monooxygenase activity; IEA.  
 DR CO; GO:0006118; P:electron transport; IEA.  
 DR InterPro; IPR000759; Adrindrk\_reductase.  
 DR InterPro; IPR001327; FAD\_Pyr\_redox.  
 DR InterPro; IPR000960; Flav\_cont\_mnoxgn.  
 DR InterPro; IPR000205; NAD\_Bs.  
 DR InterPro; IPR000205; NAD\_F.  
 DR PFam; PF00743; FMO-like\_1.  
 DR PRINTS; PRO0419; ADXNDTASE.  
 DR PRINTS; PRO0368; FADPNR.  
 DR PRINTS; PR00370; FMXYGENASE.  
 DR SEQUENCE 470 AA; 53837 MW; 6345C99AE5110919 CRC64;  
 Query Match 59.5%; Score 47; DB 10; Length 470;  
 Best Local Similarity 77.8%; Pred. No. 9.3; 0; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 0; Mismatches 0;  
 Sq Qy 3 CCGYKLCP 11  
 Db 283 CTGKYKCFP 291

[2] RESULT 15  
 RN Q9LE85 PRELIMINARY;  
 ID Q9LE85 PRELIMINARY;  
 AC DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
 DE Hypothetical protein.  
 GN AT4G11540.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophytina; Tracheophyta;  
 OC Spermatophytina; Magnoliophytina; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 NCBI\_TaxID=3702;  
 [1] RN SEQUENCE FROM N.A.  
 RP EU Arabidopsis sequencing project.  
 RA Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP Lennard N., Quail M., Harris B., Rajandream M.A., Barrell B.G.,  
 RA Mewes H.W., Lemke K., Mayer K.F.X.;  
 RA Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.  
 RL DR EMBL; AL050399; CAB82159.1; -.  
 DR EMBL; AL161532; CAB8197.1; -.  
 PIR; TI10574; TI10574;  
 DR PIR; TI10574; TI10574;  
 DR GO; GO:0005489; F:electron transporter activity; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR GO; GO:0007242; P:intracellular signaling cascade; IEA.  
 DR InterPro; IPR000345; CycC\_heme\_BS.  
 DR InterPro; IPR002219; DAG\_P-E-bind.  
 DR InterPro; IPR004146; DC1.  
 DR PFam; PF03107; DC1; 3.  
 DR SMART; SM00109; C1; 4.  
 DR PROSITE; PS00190; CYTOCHROME\_C; 2.  
 KW HYPOTHETICAL PROTEIN.  
 SQ SEQUENCER 525 AA; 60740 MW; 069557044AB56D4A CRC64;  
 Query Match 59.5%; Score 47; DB 10; Length 525;  
 Best Local Similarity 77.8%; Pred. No. 10;